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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12Q 1/68	A2	(11) International Publication Number: WO 00/52204 (43) International Publication Date: 8 September 2000 (08.09.00)
<p>(21) International Application Number: PCT/IB00/00367</p> <p>(22) International Filing Date: 22 February 2000 (22.02.00)</p> <p>(30) Priority Data: 60/121,124 22 February 1999 (22.02.99) US</p> <p>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/121,124 (CON) Filed on 22 February 1999 (22.02.99)</p> <p>(71)(72) Applicant and Inventor: ORNTOFT, Torben, F. [DK/DK]; Dept. Clin. Biochem, Skejby Sygehus, DK-8200 Aarhus N (DK).</p> <p>(74) Agent: JANSSEN, Bernd; Uexküll & Stolberg, Beselerstrasse 4, D-22607 Hamburg (DE).</p>	<p>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>Without international search report and to be republished upon receipt of that report.</i></p>	
<p>(54) Title: GENE EXPRESSION IN BLADDER TUMORS</p> <p>(57) Abstract</p> <p>Methods for analyzing tumor cells, particularly bladder tumor cells employ gene expression analysis of samples. Gene expression patterns are formed and compared to reference patterns. Alternatively gene expression patterns are manipulated to exclude genes which are expressed in contaminating cell populations. Another alternative employs subtraction of the expression of genes which are expressed in contaminating cell types. These methods provide improved accuracy as well as alternative basis for analysis from diagnostic an prognostic tools currently available.</p>		

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GENE EXPRESSION IN BLADDER TUMORS

This application claims the benefit of U.S. Provisional Application No. 60/121,124, filed February 22, 1999, which is hereby incorporated by reference in its entirety.

5 TECHNICAL FIELD OF THE INVENTION

This invention is related to the field of cancer diagnosis and treatment. In particular it is related to the use of gene expression to categorize and detect tumors.

BACKGROUND OF THE INVENTION

10 The building of large databases containing human genome sequences is the basis for studies of gene expressions in various tissues during normal physiological and pathologic conditions. Constantly (constitutively) expressed sequences as well as sequences whose expression is altered during disease processes are important for our understanding of cellular properties, and for
15 the identification of candidate genes for future therapeutic intervention. As the number of known genes and ESTs build up in the databases, array-based simultaneous screening of thousands of genes is necessary to obtain a profile of transcriptional behaviour, and to identify key genes that, either alone or in combination with other genes, control various aspects of cellular life. One

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Still another object of the invention is to provide a method of identifying a tissue sample as urothelial.

Yet another object of the invention provides a method of determining an expression pattern of a bladder tissue sample independent of the proportion of submucosal, muscle, and connective tissue cells present.

These and other objects of the invention are achieved by providing one or more of the embodiments described below. In one embodiment a method is provided of determining an expression pattern of a cell sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present. Expression is determined of one or more genes in a sample comprising cells. The one or more genes exclude genes which are expressed in the submucosal, muscle, and connective tissue. A pattern of expression is formed for the sample which is independent of the proportion of submucosal, muscle, and connective tissue cells in the sample.

In another aspect of the invention a method of determining an expression pattern of a cell sample is provided. Expression is determined of one or more genes in a sample comprising cells. A first pattern of expression is thereby formed for the sample. Genes which are expressed in submucosal, smooth muscle, or connective tissue cells are removed from the first pattern of expression, forming a second pattern of expression which is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the sample.

Another embodiment of the invention provides a method for determining an expression pattern of a urothelium or bladder cancer cell. Expression is determined of one or more genes in a sample comprising urothelium or bladder cancer cells; the expression determined forms a first pattern of expression. A second pattern of expression which was formed using the one or more genes and a sample comprising predominantly submucosal, smooth muscle, or connective tissue cells, is subtracted from the first pattern of expression, forming a third pattern of expression. The third pattern of expression reflects expression of the urothelium or bladder cancer cells

independent of the proportion of submucosal, smooth muscle, or connective tissue cells present in the sample.

5 In another embodiment of the invention a method is provided of detecting an invasive tumor in a patient. A marker is detected in a sample of a body fluid. The body fluid is selected from the group consisting of blood, plasma, serum, urine, ascites fluid, pleural fluid, spinal fluid, sputum, and mucous secretions. The marker is an mRNA or protein expression product of a gene which is more prevalent in submucosal, smooth muscle, or connective tissue than in the body fluid. An increased amount of the marker in the body
10 fluid indicates a tumor which has become invasive in the patient.

In another aspect of the invention a method is provided for diagnosing a bladder cancer. A first pattern of expression is determined of one or more genes in a bladder tissue sample suspected of being neoplastic. The first pattern of expression is compared to a second and third reference pattern of
15 expression. The second pattern is of the one or more genes in normal urothelium and the third pattern is of the one or more genes in bladder cancer. A first pattern of expression which is found to be more similar to the third pattern than the second indicates neoplasia of the bladder tissue sample.

According to yet another aspect of the invention a method is provided
20 for predicting outcome or prescribing treatment of a bladder tumor. A first pattern of expression is determined of one or more genes in a bladder tumor sample. The first pattern is compared to one or more reference patterns of expression determined for bladder tumors at a grade between I and IV. The reference pattern which shares maximum similarity with the first pattern is
25 identified. The outcome or treatment appropriate for the grade of tumor of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

In another embodiment of the invention a method is provided for determining grade of a bladder tumor. A first pattern of expression is
30 determined of one or more genes in a bladder tumor sample. The first pattern is compared to one or more reference patterns of expression determined for

bladder tumors at a grade between I and IV. The reference pattern which shares maximum similarity with the first pattern is identified. The grade of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

5 Yet another embodiment of the invention provides a method to determine stage of a bladder tumor. A first pattern of expression is determined of one or more genes in a bladder tumor sample. The first pattern is compared to one or more reference patterns of expression determined for bladder tumors at different stages. The reference pattern which shares
10 maximum similarity with the first pattern is identified. The stage of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

In still another embodiment of the invention a method is provided for identifying a tissue sample as urothelial. A first pattern of expression is
15 determined of one or more genes in a tissue sample. The first pattern of expression is compared to a second pattern of expression obtained from normal urothelial cells. Similarity between the first and second patterns identifies the tissue sample is urothelial in its origin.

Another aspect of the invention is a method to identify a set of genes
20 useful for diagnosing, predicting outcome, or prescribing treatment of a bladder cancer. A first pattern of expression is determined of one or more genes in a first bladder tissue sample. A second pattern of expression is determined of the one or more genes in a second bladder tissue sample. The first bladder tissue sample is a normal urothelium sample or an earlier stage or lower grade of
25 bladder tumor than the second bladder tissue sample. The first pattern of expression is compared to the second pattern of expression to identify a first set of genes whose expression is increased or decreased in the second bladder tissue sample relative to the first bladder tissue sample. Those genes which are expressed in submucosal, smooth muscle or connective tissue are removed
30 from the first set of genes to produce a second set of genes. Expression of the

second set of genes can be used for diagnosing, predicting outcome, or prescribing treatment of a bladder cancer.

According to yet another aspect of the invention a method is provided for determining an expression pattern of a bladder tissue sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present. A single-cell suspension of disaggregated bladder tumor cells is isolated from a bladder tissue sample comprising bladder cells, submucosal cells, smooth muscle cells, or connective tissue cells. The expression of one or more genes in the single-cell suspension is determined. A pattern of expression is thus formed for the sample which is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the bladder tissue sample.

According to still another aspect of the invention a method is provided for screening compounds to identify candidate therapeutic agents for treating bladder cancer. Bladder tumor cells are contacted with a test compound. Gene expression of one or more genes is determined in the bladder tumor cells which have been contacted with the test compound. The one or more genes are ones whose expression changes during the development of a bladder cancer. A test compound is identified as a candidate therapeutic agent if it causes gene expression of at least one of the one or more genes to change to a level which is characteristic of an earlier stage of cancer progression.

The present invention thus provides the art with numerous methods for molecularly assessing bladder cells. The methods aid the art in diagnosing, identifying, classifying, treating, detecting, and treating tumors of the bladder.

BRIEF DESCRIPTION OF THE DRAWINGS AND TABLES

Figure 1 shows a distribution of expression levels in bladder wall tissue expressed in arbitrary units. Only genes scored as present or marginally present are shown.

Figure 2 shows a comparison of intensity differences between a tumor and a pool of tumors of the same stage and grade, and two pools of different

stages and grades. The difference is larger between the pools, demonstrating the validity of using expression patterns to determine stage, grade, prognosis, and treatment regimen.

5 All genes scored as present on two chips (approximately 9000 genes) were compared. Increased genes were compared to increased genes and decreased genes to decreased genes, on two separate chips, followed by plotting of the numerical difference of the medians. A TaGrII tumor compared to the TaGrII pool, and the TaGrII pool to T2GrIV pool (1, 2, 3, 4); T2GrIII to T2GrIII pool, and T2GrIII pool to T2GrIV pool (5, 6, 7, 8); T2GrIV to 10 T2GrIV pool, and T2GrIV pool to TaGrII pool (9, 10, 11, 12). Paired T-test of medians showed a borderline significant difference, with pool vs. pool scoring highest (P-value of 0.07).

Figure 3 shows progression of a bladder cancer from normal urothelium to invasive grade IV tumor. The expression patterns change during the 15 progression, with a great variation in pattern from stage to stage, but also within a stage and even within tumors having the same stage and grade of atypia.

Figure 4 shows the correlation between transcript levels from genes expressed in at least one sample. Fig. 4A demonstrates the repeatability of 20 microarray expression analysis. Duplicate determinations on a normal sample are compared. Fig. 4B is a plot of a pTa tumor vs. the normal pool. Fig. 4C is a plot of an invasive pT2 tumor versus the normal pool. The vast majority of transcripts are present at similar levels in both normal and tumor tissue.

Figure 5 shows dendrograms of tissues based on different clustering 25 methods. Clustering was either based on log-fold change in expression level of genes (Figs. 5A, 5C), or the absolute difference (Figs. 5B, 5D), comparing tumor to a pool of normal samples. Genes used for clustering were either those 10% of the genes that covaried best with progression (A, B), or all 4076 genes that were scored as present in at least one sample (C, D).

30 Figure 6A through 6F show how the pattern of expression changes during progression of bladder cancer based on levels of transcripts in pools of

normal biopsies, superficial pTa tumors grade II, and invasive pT2+grade IV tumors. The curve at the top left portion of each subfigure shows the direction of change in gene expression based on pools of normal urothelium (open circle), superficial pTa tumor (gray circle) and invasive pT2+ tumor (black circle). Fold change in gene expression level was calculated on a probe-to-probe basis using 20 probes per gene and eliminating the highest and lowest outliers (olympic scoring). It is noteworthy that reduced expression is the most common event.

Figure 7 shows a cluster diagram of 9 bladder tumors representing the progression of bladder cancer. Each column represents a tumor preparation, and each row a gene. The diagrams show clustering based on log-fold change from normal urothelium (left diagram) and based on absolute difference from normal urothelium (right diagram). A decreased expression is displayed as shades of cyan, an increased expression as shades of yellow, and no change as black.

The dendrograms at each side show the relation between the different genes. In the middle, distinct functional clusters are identified and members of the clusters are annotated in brief (for full length ID of all genes in the diagram and Genbank numbers see www.mdl.dk/supplementary data). In an effort to identify those genes most indicative of cancer progression a weighting scheme was used to select the 400 genes that covaried best with the different stages of bladder cancer. Gene clustering was based on normalized Euclidean distance (vector angle) calculated between genes or gene cluster centers.

Figure 8 shows the vector angle between pools and individual single cell preparations or biopsies. The numbers refer to patient samples and the stage of each is indicated. Pools are identified as follows: squares, Ta grade I pool; diamonds, Ta grade II pool; circles, T2-4 grade III pool; triangles, T2-4 grade IV pool. The lowest angle for each sample determines the whether the sample is classified as a superficial (Ta or T1) or muscle-invasive tumor (T1-T4).

Figure 9 shows a comparison of Northern blots and oligonucleotide arrays. The samples analyzed were normal pool (Norm), superficial pTaGrI tumor (335), minimally invasive pT1 grade III (901), and invasive pT2 grade III (713). The Northern blots were scanned by densitometry and plotted (solid lines) together with a plot of the level detected on the arrays (dotted lines). The levels of expression ranged from 3-6,000 units (beta -2 microglobulin) to 100-600 units (E-cadherin). The level of transcripts detected was similar with both methods.

Figure 10 shows immunohistochemical staining of the tissue sections used for expression analysis. On each section the protein examined is indicated and the level measured on the oligonucleotide array. Arrows indicate stained urothelial cells in cathepsin E (297 arbitrary units), ApoE (389 units), and CD59 (260 units) stainings, and stained stromal cells or leukocytes in beta2-microglobulin (2481 units) and cystatin C (941 units).

Figure 11 presents a model of gene expression events during the progression of bladder cancer. The top of the figure shows the stages of bladder cancer, and the lower part shows the sequence of transcriptional events. The color cyan identifies reduced expression, yellow increased expression (also indicated by arrows). The figure is based on data from cluster analysis, and combines the different cluster methods.

Table I shows genes which were highly expressed in bladder wall. Expression is shown in "connective tissue" which includes muscle and submucosal cells, a TaGr III, a T₂Gr III, and a T₂Gr IV bladder tumor. Genes above the 90th percentile are grouped according to the purported function of the protein.

Table 2A shows high intensity genes in bladder wall compared to single cell solutions and biopsies of tumors.

Table 2B shows expression of genes related to bladder wall.

Table 3 shows the number of genes that are expressed as in the tumor-pool to which the tumor belongs, or altered as in a tumor pool of higher or lower stage or grade.

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Several of the tables described above contain lists which include both genes and expressed sequence tags (ESTs). Reference to the "genes" of a table shall be understood to include the gene containing the EST.

DETAILED DESCRIPTION OF THE INVENTION

5 It is a discovery of the present inventor that characteristic patterns of expression of genes can be used to characterize different types of tissue. Thus, for example, gene expression patterns can be used to characterize stages and grades of bladder tumors. Similarly, gene expression patterns can be used to distinguish cells having a bladder origin from other cells. Moreover, gene
10 expression of cells which routinely contaminate bladder tumor biopsies has been identified, and such gene expression can be removed or subtracted from patterns obtained from bladder biopsies. Further, the gene expression patterns of single-cell solutions of bladder tumor cells have been found to be far freer of interfering expression of contaminating muscle, submucosal, and connective
15 tissue cells than biopsy samples.

 Working with human tumor material requires biopsies, and working with RNA requires freshly frozen or immediately processed biopsies. Biopsies inevitably contain many different cell types in addition to cancer cells, such as cells present in blood, connective and muscle tissue, endothelium etc. In the
20 case of DNA studies, microdissection or laser capture are methods of choice, however, the time-dependent degradation of RNA makes it difficult to perform manipulation of the tissue for more than a few minutes. Furthermore, studies of expressed sequences may be difficult on the few cells obtained via microdissection or laser capture, as these may have an expression pattern that
25 deviates from the predominant pattern in a tumor due to intratumoral heterogeneity.

 High-density expression arrays were used to evaluate the impact of bladder wall components in bladder tumor biopsies, and tested preparation of single cell solutions as a means of eliminating the contaminants. The results of
30 these evaluations permitted the design of methods of evaluating bladder

samples without the interfering background noise caused by ubiquitous contaminating submucosal, muscle, and connective tissue cells.

The evaluating assays of the invention may be of any type. While high-density expression arrays can be used, other techniques are also contemplated. These include other techniques for assaying for specific mRNA species, including RT-PCR and Northern Blotting, as well as techniques for assaying for particular protein products, such as ELISA, Western Blotting, and enzyme assays. Gene expression patterns according to the present invention are determined by measuring a gene product of a particular gene, including mRNA and protein. A pattern may be for one or more genes.

Using the results provided in the accompanying figures and tables, a gene is indicated as being expressed if an intensity value of greater than or equal to 21 is shown. Conversely, an intensity value of less than 21 indicates that the gene is not expressed above background levels. Comparison of an expression pattern to another may score a change from expressed to non-expressed, or the reverse. Alternatively, changes in intensity of expression may be scored, either increases or decreases. Any statistically significant change can be used. Typically changes which are greater than 2-fold are suitable. Changes which are greater than 3-fold or 5-fold are highly significant.

A pattern of characteristic expression of just one gene can be useful in characterizing a cell type source or a stage of disease. However, more genes may be usefully analyzed. Useful patterns include expression of at least one, two, three, five, ten, fifteen, twenty, twenty-five, fifty, seventy-five, or one hundred informative genes. As used herein, the phrase "stage-specific reference pattern" refers to a pattern of gene expression characteristic of a given stage of progression in a bladder tumor. A stage-specific reference pattern can include one or more genes listed in Table 4 and/or one or more genes listed in Table 8 and/or one or more genes listed in Table 9 and/or one or more genes listed in Fig. 6.

RNA or protein can be isolated and assayed from a test sample using any techniques known in the art. They can, for example, be isolated from fresh

or frozen biopsy, from formalin-fixed tissue, from body fluids, such as blood, plasma, serum, urine, or sputum.

5 Stage of a bladder tumor indicates how deeply the tumor has penetrated. Superficial tumors are termed Ta, and T₁₋₄ are used to describe increasing degrees of penetration into the muscle. The grade of a bladder tumor is expressed on a scale of I-IV (1-4). The grade reflects the cytological appearance of the cells. Grade I cells are almost normal. Grade II cells are slightly deviant. Grade III cells are clearly abnormal. And Grade IV cells are highly abnormal.

10 As used herein, the reference to genes which are expressed in "submucosal, smooth muscle, or connective tissue" or patterns of expression in "other cell types" can include the expression of one or more of the genes listed in Table 1 and/or one or more of the genes listed in Table 6. The term "connective tissue cell" includes any stromal cell such as fibroblasts,
15 macrophages, mast cells, granulocytes, etc. The data provided herein of expression for submucosal, smooth muscle, and connective tissue can be used in at least three ways to improve the quality of data for a tested sample. The genes identified in the data as expressed can be excluded from the testing altogether or tested but eliminated from the analysis. Alternatively, the
20 intensity of expression of the genes expressed in the submucosal, smooth muscle, and/or connective tissue can be subtracted from the intensity of expression determined for the test tissue.

 Patterns can be compared manually (by a person) or by a computer or other machine. An algorithm can be used to detect similarities and differences.
25 The algorithm may score and compare, for example, the genes which are expressed and the genes which are not expressed. Alternatively, the algorithm may look for changes in intensity of expression of a particular gene and score changes in intensity between two samples. A variety of such algorithms are known in the art. Similarities may be determined on the basis of genes which
30 are expressed in both samples and genes which are not expressed in both samples or on the basis of genes whose intensity of expression are numerically

similar. Differences are considered significant when they are greater than 2-fold, 3-fold or 5-fold from the base value. Alternatively, a mathematical approach can be used to conclude whether differences in the gene expression exhibited by different samples is significant (*see, e.g.*, Golub et al., Science 286, 531 (1999)). One approach to determine whether a sample is more similar to
5 or has maximum similarity with a given condition (*e.g.*, a particular grade or stage of tumor progression) is to compare the Euclidean distances (*see* Golub et al. and Example 6) between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is
10 then chosen as the most similar to the test sample among the pools compared.

The data collected and disclosed here as "connective tissue" is presumed to contain both smooth muscle and submucosal gene expression as well. Thus it represents the composite expression of those cell types which can typically contaminate a bladder tumor biopsy.

15 Genes identified as changing in various stages or grades of bladder cancer can be used as markers for drug screening. Thus by treating bladder cancer cells with test compounds or extracts, and monitoring the expression of genes identified as changing in the progression of bladder cancers, one can identify compounds or extracts which change expression of genes to a pattern
20 which is of an earlier stage/grade or even of normal urothelium. As used herein, the reference to expression of genes in "normal urothelium" or "normal urothelial cells" can include one or more genes listed in Table 7.

As demonstrated below, pools of tumors of a similar stage or grade, particularly bladder tumors, can be made and the expression of the pool
25 evaluated. The expression data of the pool can be used to define a stage or grade of tumor. The use of the pool minimizes the variations found from individual tumor to individual tumor of the same grade or stage. The expression data of the pool can then be used as a comparator to which individual tumor samples are compared, in an effort to categorize,
30 prognosticate, and prescribe the tumor samples. The methods described herein for classifying the stage or grade of a tumor can be combined with sequence

analysis of genes whose expression is altered compared to normal tissue in the individual patient. In particular, mutations in key genes such as tumor suppressor genes can help to refine the application of the gene expression results to diagnosis and prognosis.

5 As used herein, the reference to expression of "genes in bladder cancer" or "genes in a bladder tumor" can include one or more genes listed in Table 4 and/or one or more of the genes listed in Table 8 and/or one or more genes listed in Table 9.

10 The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

Quantification of gene expression using microarrays

15 Material

Bladder tumor biopsies were sampled from patients after informed consent was obtained, and after removal of the necessary amount of tissue for routine pathological examination. Tumors examined were 335 (stage pTa grade I), 837 (pTa GrII), 901 (pTa GrIII), 320 (pT1 GrIII), 713 (pT2 GrIII).
20 RNA from six different tumors of the same stage and grade was combined to form each pool. Four such pools were prepared (pTa GrI pool, pTa GrII pool, pT2+ GrIII pool, and pT2+ GrIV pool). Normal bladder mucosa biopsies from 36 patients with prostatic hyperplasia or incontinence were pooled (as RNA) to obtain a normal urothelial reference. Single cell solutions were made by
25 disintegrating biopsies on ice with a scalpel and a syringe followed by filtering through a 50 micron filter.

Preparation of mRNA

Total RNA was isolated using the RNeasy RNeasy spin protocol (Qiagen) (WAK-Chemie Medical GMBH). Poly (A)+ RNA was isolated by an oligo-dT
30 selection step (Oligotex mRNA kit from Qiagen).

Preparation of cRNA

One µg mRNA was used as starting material for the cDNA preparation. The first and second strand cDNA synthesis was performed using the SuperScript Choice System (Life Technologies) according to the manufacturer's instructions, except that an oligo-dT primer containing a T7 RNA polymerase promoter site was used. Labeled cRNA was prepared using the MEGAscrip In Vitro Transcription kit (Ambion). Biotin labeled CTP and UTP (Enzo) was used in the reaction together with unlabeled NTP's. Following the IVT reaction, the unincorporated nucleotides were removed using RNeasy columns (Qiagen).

Array hybridization and scanning

Ten µg of cRNA was fragmented at 94°C for 35 min. in a fragmentation buffer containing 40mM Tris-acetate pH 8.1, 100mM KOAc, 30 mM MgOAc. Prior to hybridization, the fragmented cRNA in a 6xSSPE-T hybridization buffer (1M NaCl, 10mM Tris pH 7.6, 0.005% Triton) was heated to 95°C for 5 min and subsequently to 40°C for 5 min before loading onto an Affymetrix probe array cartridge (HuGeneF1 set array, part No. V900160). The probe array was then incubated for 16 h at 40°C at constant rotation (60 rpm). The washing and staining procedure was performed in the Affymetrix Fluidics Station. The probe array was exposed to 10 washes in 6xSSPE-T at 25°C followed by 4 washes in 0.5xSSPE-T at 50°C. The biotinylated cRNA was stained with a streptavidin-phycoerythrin conjugate, 10 µg/ml (Molecular Probes, Eugene, OR) in 6xSSPE-T for 30 min at 25°C followed by 10 washes in 6xSSPE-T at 25°C. The probe arrays were scanned at 560 nm using a confocal laser scanning microscope with an argon ion laser as the excitation source (made for Affymetrix by Molecular Dynamics). The readings from the quantitative scanning were analyzed by the Affymetrix Gene Expression Analysis Software.

Normalization of data

To compare samples, normalization of the data was necessary. For that purpose we compared scaling to total GAPDH intensity (sum of 3', middle,

5'probe sets) of 7000 units with scaling to a total chip intensity (global scaling) of 281850 units (averaging 150 units per probe set). Both gave similar results with scaling factors that differed less than ten percent in a set of experiments. Based on this we chose the global scaling for all experiments. The variation in hybridization intensity following global scaling in biopsies from the bladder wall is shown in Fig.1.

EXAMPLE 2

Interference of bladder wall components on expression profiling of bladder tumor biopsies

10 Biopsies contain epithelial cells that most often are the targets for the studies (e.g., in the identification and characterization of carcinoma cells), and in addition many other cells that contaminate the epithelial cell fraction to a varying extent. The contaminants include histiocytes, endothelial cells, leukocytes, nerve cells, muscle cells etc. Microdissection is the method of choice for DNA examination, but in case of expression studies this procedure is difficult due to RNA degradation during the procedure. Our approach has been to gently remove the epithelium and monitor the expression in the remaining submucosa and underlying connective tissue (the bladder wall). Genes expressed at high or low levels in the bladder wall should be interrogated when performing expression monitoring of the urothelium and urothelial tumors. A similar approach could be used for studies of epithelia in other organs.

25 We gently scraped off some of the normal urothelium lining the bladder lumen from bladders removed at cystectomy for bladder cancer. Then biopsies were taken from the denuded submucosa and connective tissue, reaching approximately 5 mm into the bladder wall, and immediately disintegrated in guanidinium isothiocyanate. Total RNA was extracted from four different cystectomy specimens, pooled, and poly(A)⁺ mRNA was prepared from the pool followed by conversion to double-stranded cDNA and in vitro transcription into cRNA containing biotin-labeled CTP and UTP.

30

The labeled sample was hybridized to a set of 4 arrays containing 7074 probe sets for human genes. A total of 1491 of the examined genes (21.1%) were scored as present, and 120 (1.7%) as present but rare. The percentile distribution of the expression intensity was (90%, 1308; 75%, 383; 50%, 163; 25%, 85; 10%, 47). Genes above the 90th percentile (Table 1) were grouped according to the purported function of the protein (Table 1, first column). Many of the highly expressed genes belong to a group of genes that encode proteins involved in transcription and translation, probably reflecting that these genes generally are highly expressed in the various cell types present in the bladder wall, and corresponding to recent data on yeast. Structural proteins such as keratins and proline rich proteins are highly expressed whereas collagen genes are only medium expressed. Extremely high expression is shown by the cystic fibrosis antigen gene, the S100 calcium binding protein, the cystatin B and the cytokeratin 13 genes that are all above 10,000 units.

To evaluate the influence of bladder wall tissue in urothelial tumor biopsies, we monitored the expression level in 3 biopsies from transitional cell carcinomas (one superficially invasive (#733-2) and two muscle invasive (#733-1 and #879-1). The expression intensity in the tumor biopsies of genes that are highly expressed in bladder wall are listed in Table 1. Many genes are expressed to the same magnitude in the tumor biopsies as in bladder wall, 82 genes (5%) were present at a level above 1308 in all samples, and above the 75% percentile of the bladder wall sample intensity (383 units) 210 genes were expressed in all three biopsies as well as in bladder wall. Genes that were not expressed in bladder wall but present in the urothelial biopsies amounted to 196.

Genes that are expressed and genes that are not expressed in bladder wall can both interfere with the interpretation of the expression in a biopsy, and should be interrogated when interpreting expression intensities in urothelial tumor biopsies, as the bladder wall component of a biopsy varies in amount from biopsy to biopsy.

It is remarkable how similarly many genes belonging to the groups encoding metabolically active proteins, transcription and translation related proteins, mitochondrial and nucleoproteins, are expressed in the different samples (Table 1). It seems reasonable to expect that it is incompatible with
5 cellular function to stray from a narrow interval regarding these genes. Although some of the examined cells are malignant of atypia grade IV, which is a severe morphological deviation from normal, the key cellular functions are obviously still under strict control.

Twenty six genes were expressed at an intensity above 1308 in bladder
10 wall and more than five times lower in tumor biopsies. These genes, marked with bold (Table 1), include keratins (7 genes) encoding proteins like keratins type II, 4, and 6. Another prominent group are the genes encoding proline-rich proteins (5 genes). These gene expressions can be used to monitor the amount of bladder wall present in a given biopsy of tumors. The tumor biopsy 879-1
15 obviously has a larger bladder wall component than the other biopsies, as it contains keratin 13 and several other highly expressed bladder wall mRNAs at a low level, but higher than the other specimens (Table 1).

An interesting result was the S100 calcium binding protein A7 gene transcript that was highly expressed in bladder wall and totally absent from the
20 other biopsies (also absent from a number of other examined tumor biopsies from bladder). As all samples were collected with the same procedures, it indicates that this expression is either individual and occurred by chance in the patients from whom we removed the bladder wall biopsies, or, more likely, that the presence of urothelial RNAases degrade this transcript very fast.

25 Bladder tumors have a reduced intercellular cohesion, and easily disintegrate into single cell solutions. To eliminate bladder wall cells from the urothelial tumor cells, five tumors were disintegrated into single cell solutions before extraction of RNA, and compared to three tumors where RNA was extracted from the biopsy directly. We expected that this disintegration
30 procedure might lead to an enrichment of tumor cells and loss of connective tissue cells. Examination of genes highly expressed in bladder wall (Table 2A),

showed a similar expression in single cell solutions of bladder tumor cells compared to biopsies. However, the level was much lower than seen in the bladder wall and raised the question whether the expressed RNAs originate from the bladder wall or from the urothelial cells.

5 To answer this question we examined the expression of genes expected to be present in bladder wall (Table 2B). Some of these genes were expressed in the bladder tumor samples, and probably indicate the presence of bladder wall components in these. It was striking that the single cell solutions contained much lower expression levels of these genes compared to the biopsies
10 ($p < 0.004$). Although the number of examined tumors was small this indicates that preparation of single cell solutions may reduce the presence of bladder wall cells in the samples. The absence of keratin 8 in the bladder wall sample demonstrated that this sample was devoid of urothelial cells (Table 2B).

15 The genes known to be related to the bladder wall components, showed a variable level throughout the samples. Some genes like myosin light chain 2 gene, fibroblast tropomyosin gene and alpha-1 collagen type IV gene, were generally more expressed in the tumor samples than the other genes (Table 2B). We hypothesize that this may reflect that there is a differential expression of genes in the connective tissue component that inevitably is included in a
20 tumor biopsy, an expression that may deviate from the one found in the bladder wall further away from the tumor. An example of this differential expression in bladder wall was the presence of transcript from the myosin light chain gene in the tumor samples but not in the bladder wall biopsies (Table 2B).

25 In tumors many important events take place in the non-epithelial compartment. Tumors need a connective tissue support, they need blood vessels, they interact with the immune system and have intercellular signaling with various sorts of other cells in a complicated way that has not yet been clarified in detail. Gene expression originating from the non-epithelial compartment contributes to the expression profile of a tumor, and might be of
30 great importance in relation to the clinical outcome and therapeutic response of the tumor.

EXAMPLE 3

Expression profiling of tumor pools to assess individual tumor heterogeneity.

We expected tumors from the same pathology stage and grade to have a more similar gene expression than tumors from different stages and grades. This was the case; however, these differences were not striking, and there were exceptions. Based on this we hypothesized that, a given tumor scored by a pathologist at light microscopy to be similar to another one may actually represent tumors with a remarkably different gene expression. The reason for this could be that tumors do not progress from a well defined stage to another well defined stage, but rather that a continuous change is taking place at the expression level -- which is then only partly reflected by morphology.

We tested this hypothesis by examining the expression which differed between a pool of tumors from a given stage and a single tumor, to see whether the differentially expressed genes were linked to a certain stage or whether they were a random deviation. It was evident that tumor expression that deviates from the pool systematically have expressions belonging to either a lower or a higher stage, or both, or unique expressions not seen in the pool (Fig. 3). The low stage Ta tumor had 43 genes whose expressions were increased or decreased similar to the ones seen in a Stage 2 grade IV tumor pool, and only three expressions that were altered in the opposite direction of stage 2 grade IV. The stage 2 grade IV tumor had 33 genes whose expression was either increased or decreased similar to the ones seen in the Ta superficial tumor pool, and only 8 genes altered in the opposite direction. In the T2 grade III tumor, gene expressions that were increased or decreased similar to the superficial or the grade IV invasive pool could be found. Furthermore some gene expressions were only low in this grade III tumor, and higher in both superficial and grade IV tumor pools. The clinical information on the examined single tumors (Table 3) paralleled the expression findings as the intermediate grade III tumor was the first muscle invasive tumor in a patient who had had a superficial tumor five months earlier. It seems that this tumor has not reached the level of malignancy as seen in the other invasive tumor. The latter was of

grade IV, and was a big solid tumor with muscle invasion at first visit. The superficial Ta tumor was the fifth recurrence and was followed by two new recurrences 64 and 159 days later--also of superficial nature.

5 The genes that were identified in lower stage and grade tumors and shown to be similar to the expression in high stage tumors are listed in Tables 4A and 4B. These genes may "signal" a higher stage or grade, or represent a transition from low stage or grade to high stage or grade. To aid in avoiding interpreting bladder wall expression as tumor cell-specific expression, the expression level in bladder wall is listed in Tables 4A and 4B. Two columns
10 are shown which simulate an increase in bladder wall content to 20% and 50% of the sample. These columns were obtained by adding a 20% or 50% contribution from the "bladder wall" column to the appropriate remaining percentage contribution (80% or 50%) from the TaGrII Pool column. Single tumor expression level (column labeled "Ta single tumor") was interrogated in
15 this context. Expression levels which are unlikely to be due to bladder wall contamination are shown in bold; other expressions are shown in regular font. We believe this procedure is useful and leads to reliable conclusions.

These genes form a complex group of genes with highly different functions. It is not totally unexpected that mucin synthesis is changed, nor that
20 cytokeratin 15 is decreased when moving from Ta and to higher stage. The gene expressions which signal a higher grade of atypia in already invasive grade III tumors are, among others, immunology related genes. This may indicate that the more atypical cells are either surrounded by inflammatory cells, or that the tumor cells start synthesizing these proteins. Further investigation is needed
25 to elucidate this point, and these proteins will be an interesting parameter to follow in relation to clinical course in the future. The strong up-regulation of cathepsin B may indicate an increased proteolytic attack against the connective tissue.

The cause of the changed expression is unknown and could be either
30 a transcriptional regulation or secondary to gain or loss of chromosome material. Both mechanisms are known to occur in cancer cells.

EXAMPLE 4

Change of transcript level during the progression of bladder cancer.

Biopsies from human bladder tumors were analyzed as single tumors or as pools of tumors representing the different stages in the progression of the bladder cancer disease. We used a total of 5 single tumors and 4 tumor pools, each pool made by combining six tumors. To generate a normal reference material, we pooled biopsies from normal bladder mucosa from 35 volunteers. The biopsies were disintegrated into single cell solutions immediately after removal, filtered and snap frozen in guanidinium isothiocyanate. From the cell solutions RNA was extracted, reverse transcribed to cDNA and the cDNA transcribed into labelled cRNA, that was incubated on the chip cartridges followed by scanning and scaling to a global chip intensity amounting to 150 units per probe set. The scaling made it possible to compare individual experiments to each other. To verify the reproducibility, double determinations were made in selected cases and showed a good correlation (Fig. 4A).

We compared gene expression at three different steps in the progression of bladder cancer to each other by the use of the normal pool as a reference. A scatter plot of the noninvasive pTa grade one tumor and the invasive highly abnormal grade four pT2+ tumor showed a minor subfraction of the gene transcripts to deviate much from those in the normal urothelium. The large majority of transcripts were within a narrow range in both tumors and normal urothelium (Fig. 4B,C). The number of deviating genes was higher in the most abnormal tumor.

We then analyzed transcripts that showed alterations larger than five-fold, when comparing three different pools representing the transition from normal urothelium to superficial tumor, and further on to invasive transitional cell carcinomas (TCC). The method applied consisted in a probe-to-probe comparison (20 probes per gene) based on the software GeneChip® Analysis Suite 3.1 from Affymetrix, Inc. Increased levels indicate that the transcript is either upregulated at the stated level or turned on *de novo* reaching a given fold above the background level. Decreased levels in a similar way indicate

reduction or loss of transcript. Alterations of a single transcript during the progression of the bladder cancer disease can follow several different pathways (Fig. 6). Some of the transcript changes reflect the transition from normal cells to tumor cells, and are grouped as *TCC related genes* (Fig. 6A, B). A distinct feature of group A was the presence of 6 smooth muscle related genes. Others are altered only in superficial tumors, not in invasive tumors, and are grouped as *Bladder papilloma related genes* (Fig. 6C, D). Group C, with downregulated genes, contained 15 immunology-related genes. Group D contained a variety of genes encoding proteins with different functions. Finally some genes only showed an alteration in invasive tumors and are grouped as *Invasive TCC related genes* (Fig. 6E, F). The genes in group E encoded functionally unrelated proteins, whereas group F contained 5 immunology-related genes. Thus, it seemed possible to define groups of genes whose expression level is associated with the stage of bladder tumors.

EXAMPLE 5

Cluster Analysis

The level of a gene transcript during disease progression can be thought of as a pattern that can be correlated to patterns of other gene transcripts. If the expression of one gene is very similar to the expression of another gene in several samples they are a correlated pair of genes. This pair of genes can then be correlated to other genes with a similar transcriptional behavior in the set of tissues examined, and together these constitute a gene cluster. In the next step the relation between clusters is established and a dendrogram of genes is formed, in which strongly correlating gene clusters are near each other. The principles are described in Eisen et al., Proc. Natl. Acad. Sci. USA 95, 14863 (1998). Briefly, each gene vector was placed in its own cluster, where the cluster prototype was set to the gene vector. All pair-wise vector angles between cluster prototypes were calculated. The smallest vector angle was identified, and those clusters were merged as a weighted average of the two prototypes (and also a weighted average of all the gene vectors each prototype represented). The vector angles were then updated between the newly merged

clusters and the merger process was repeated. The final clusters are displayed in the order in which they were merged.

Exactly the same procedure used to cluster genes can be used to cluster the tissue samples, showing the relation between the different tissues based on their gene expression. We based clustering analysis on either the 4067 transcripts being scored as present in at least one of the samples, or based on those 400 transcripts (see Table 9) that covaried best with a weighting scheme adding increasing values to increasing stages.

The scaled AvgDif measures as calculated by the Affymetrix software were extracted for the normal pool and each of the graded tissues. Only the 4067 genes with an AbsCall of P (present) in at least one of the tissues were considered. All AvgDif measures below 20 were set to 20. For each tissue and each gene, the AvgDif from the normal pool was either subtracted, to define the "absolute difference," or divided and natural logarithm applied to define the "log-fold" relative measure. The relative expression measures for each tissue (log-fold or absolute difference) were used to cluster tissues by a hierarchical method using the Euclidean distance between tissues. Tissue dendrograms were constructed with the PHYLIP program using clustering order and distances. A weighting scheme (see Example 6) for the seven observed stages and grades of cancer was used to select 200 positively covarying and 200 negatively covarying genes with respect to progression. The same hierarchical method and a normalized Euclidean distance (vector angle) were used to cluster the top 400 positively and negatively covarying genes for both relative expression measures. Gene dendrograms were constructed by the same method as for the tissue dendrograms.

Tissue clusters

Different algorithms based on either fold change or absolute differences in transcript levels across the different samples were applied to all transcripts or only those covarying with a progression scale. Both methods were able to cluster the tissues according to the tumor's or tumor pools stage and grade of atypia in a meaningful way (Fig. 5). The two noninvasive and the two invasive

pools each clustered very closely together both using the fold change and the absolute difference, indicating a close genetic relation between these, and indicating that one effect of pooling samples is a reduction of the variation in gene expression. The single tumor preparations showed a more varied
5 distribution but still reflected the stage of the tumor. In the log-fold dendrograms (Fig. 5A, C) the superficial tumors 335, 837 and 901 cluster close to the superficial pools, but the pTa grade III tumor 901 seems closer to the superficial pools than the pTa grade II tumor 837. This may either be due to the variation in histopathological grading or due to the tumors having different
10 genetic properties. The minimally invasive pT1 grade III tumor 320 is correctly placed in between the muscle invasive and the superficial tumors, and the muscle invasive tumor 713 is placed very close to the pools of pT2+ tumors. Tumor 713 seemed to be closer to the pT2+grade IV than Grade III pool although it was histopathologically scored as grade III. In the absolute
15 difference dendrogram (Fig. 5B, D) the superficial tumors 837 and 901 are closely related to the superficial pools, the pT1 superficially invasive tumor is less related and finally the invasive tumor 713 located closest to the invasive pools. An exception was the superficial tumor pTa grade I, 335-6 that deviated from all other tumors. Whether this tumor has unique properties is unknown,
20 however it did not deviate from the expected location in the dendrograms based on fold change.

The dendrograms show that the clustering algorithms work very well, that the dataset obtained from the oligonucleotide arrays reflect the biological properties of the tumors, and that objective information on a tumor's stage and
25 grade can be obtained from mathematical analysis of gene expression data. Furthermore, it is seen that when ranking based on covariance to the progression is used to extract the top 10% covarying genes, these have a dendrogram that is almost identical to the one based on 4067 genes. We therefore used the ranking procedure when analyzing gene clusters.

Gene clusters

The data obtained from cluster analysis are presented as colored images in which genes with similar expression patterns are clustered next to each other on the vertical axis and the samples according to stage and grade on the horizontal axis (Fig. 7). The color of each cell in the tabular image represents the ratio between the sample expression of the gene in question and the expression in normal urothelium. The color saturation is directly proportional to the magnitude of the measured expression ratio, cyan indicating the lowest ratio, yellow indicating the highest ratio. Black indicates a ratio of one, a similar level of expression in tumor as in normal urothelium. The two different clustering methods, log-fold and absolute difference gave completely different clusters across the set of samples (Fig. 7).

In the log-fold based cluster analysis, the top 200 positively covarying genes can be divided into five different clusters containing functionally related genes (Fig. 7, left upper column). The cluster shown at the top contains genes related to cell proliferation such as cyclins A and E, PCTAIRE-1, and SWI/SNF. The next cluster mainly contains oncogenes and growth factors. Genes in both these clusters are expressed at a level close to that seen in normal urothelium in superficial tumors (black) and increase during disease progression (yellow). The two clusters at the lower part show a reduced expression level in the superficial tumors compared to normal (cyan) and then an increase above the normal urothelial level in invasive tumors (shades of yellow). These clusters contain a set of immunologically related genes, like different MHC's and immunoglobulins, cancer related genes like src-like kinase and Fas/Apo-1, and finally another immunologically related cluster at the bottom.

The 200 negatively covarying genes (Fig. 7, left lower column) could be divided into three different clusters based on log-fold change and function of the genes. The upper cluster contains genes related to cell adhesion like laminins, integrins and P-cadherin (Fig. 7, left lower column). They all show a reduced level of expression in the invasive tumors as evidenced by the cyan

coloring to the right. The small middle cluster contains four genes related to transcription, and finally the lowest cluster in the figure contains five proteinases, like cathepsin E (two different probe sets for the same gene) and metalloproteinase as well as a protease inhibitor. The lower clusters are characterized by an increase in level in superficial tumors (yellow) followed by a reduction to a level below normal urothelium in invasive tumors.

In the absolute difference based cluster analysis the top 200 covarying genes that showed a positive covariance contained only few clusters having a functional relation. The upper cluster (Fig. 7, right upper column) contained five genes related to cell proliferation like the microtubule-associated protein and oncoprotein 18/stathmin. The next cluster was a set of immunology related genes like MHC and LERK-2. Both these clusters showed an increased expression level in invasive tumors compared to normal urothelium. The cluster at the lower end of the figure showed a reduced level in superficial tumors and a return to normal or increased level in invasive tumors. This cluster contained many immunology-related genes like MHC, HLA and immunoglobulin genes. Finally, for genes that showed a negative covariance based on absolute difference (Fig. 7, right lower column), this was mainly due to clustering of ribosomal genes. A very tight cluster in the middle of the graph show ribosomes that are upregulated in expression in superficial tumors and downregulated or unaltered in invasive tumors. The middle ribosomal cluster is generally expressed at a lower level than in normal urothelium, whereas the cluster at the bottom of the figure is similar to the one in the middle. Other genes that seemed to cluster were a small tight cluster of immunology related genes, and two tumor inhibitors, TGF-beta superfamily protein and Sui1 in the uppermost cluster.

Thus, a pattern of altered gene transcription occurs during the progression of bladder cancer that involves a number of genes belonging to functionally different gene families. Cluster analysis identified many biologically relevant genes, and in that aspect was superior to the probe-by-probe comparison described above.

MISSING AT THE TIME OF PUBLICATION

where
$$dp(X,Y) = \sum_{i=1}^n (x_i \times y_i)$$

and
$$len(X) = \sqrt{\sum_{i=1}^n x_i^2}$$

5 After the sample had been compared in this way to each pool, invasive and non-invasive, the pool which differed from the sample by the smaller angle was determined to be the class of the sample.

Samples from ten bladder tumors were assigned by the classifier, and the results are shown in Fig. 8. The classifier was able to correctly call the presence or absence of muscle invasion in all ten samples examined (7 non-muscle invasive, 3 muscle invasive), based on categorizations made by a pathologist. To cross-validate the classification methodology, two non-invasive (Ta) and two invasive (T2) pools were compared with tumors from each of 10 patients. Since two pools were available for each stage, four possible combinations (classifier sets) of one Ta pool and one T2 pool were tested. The classification rate was calculated as the number of tumors correctly identified times 10. The results for each of the four classifier sets were averaged to obtain the data shown in Fig. 8.

EXAMPLE 7

Confirmation of microarray expression analysis by Northern blotting

20 In order to confirm the array data, Northern blotting was performed on the same samples of RNA as used for array hybridization. A standardized amount of RNA was run in each lane, followed by blotting with a labelled RNA probe, and quantitation of the band obtained (Fig. 9).

25 Total RNA, 0.5–4 µg per lane, was separated in 1.5% agarose-formaldehyde gels, transferred onto Zeta-Probe® nylon membrane (Bio-Rad) by positive pressure (Posiblotter, Stratagene) and immobilized by baking for 20 min at 120°C. The filters were hybridized with digoxigenin-labelled (DIG) RNA transcribed from 600-1000 bp PCR products containing a T7 promotor

incorporated via the antisense primers. Filters were hybridized with 10 ng probe per ml of ultrahyb™ hybridisations solution at 68°C for 16 h and washed to a stringency of 0.1x SSC at 68°C. Specific hybridization was detected by reacting the membrane with monoclonal anti-DIG antibodies conjugated with alkaline phosphatase, incubating with ECF chemifluorescence substrate (AmershamPharmacia) and scanning on a Storm 840 (Molecular Dynamics). The hybridization signals were quantified with ImageQuant 5.0 software.

As can be seen from the plots, the oligonucleotide array and the Northern blot gave similar results with the different probes, both in genes expressed at a high level (beta2-microglobulin), and those expressed at a very low level (CD59).

EXAMPLE 8

Immunohistochemical localization of expressed proteins

The biopsy samples used to study gene expression in bladder tumors contain cells other than urothelial cells, although the amount of other cells should be limited due to the use of single cell solutions. We therefore used immunostaining of tissue sections from the single tumors examined to determine which cells expressed the protein encoded by the transcript in question. We used the transcript levels to select a group of proteins supposed to show variation from sample to sample, making possible a rough correlation between level of protein detected and intensity of the transcript on the microarray.

Four µm sections were cut from paraffin-embedded tissue blocks, mounted, and deparaffinized by incubation at 80°C for 10 min, followed by immersion in heated oil at 60°C for 10 min (Estisol 312, Estichem A/S, Denmark) and rehydration. Antigen retrieval was achieved in TEG (Tris-EDTA-Glycerol) buffer using microwaves at 900 W. The tissue sections cooled in the buffer for 15 min before a brief rinse in tap water. Endogenous peroxidase activity was blocked by incubating the sections with 1% H₂O₂ for 20 min, followed by three rinses in tap water, 1 min each. The sections were then soaked in PBS buffer for 2 min. The next steps were modified from the

descriptions given by Oncogene Science Inc., in the Mouse Immunohistochemistry Detection System, XHCO1 (UniTect, Uniondale, NY, USA). Briefly, the tissue sections were incubated overnight at 4°C with primary antibody (against beta-2 microglobulin (Dako), cytokeratin 8, cystatin-C (both from Europa, US), junB, CD59, E-cadherin, apo-E, cathepsin E, vimentin, IGFII (all from Santa Cruz), followed by three rinses in PBS buffer for 5 min each. Afterwards, the sections were incubated with biotinylated secondary antibody for 30 min, rinsed three times with PBS buffer and subsequently incubated with ABC (avidin-biotinylated horseradish peroxidase complex) for 30 min, followed by three rinses in PBS buffer. Staining was performed by incubation with AEC (3-amino-ethylcarbazole) for 10 min. The tissue sections were counter stained with Mayers hematoxylin, washed in tap water for 5 min. and mounted with glycerol-gelatin. Positive and negative controls were included in each staining round with all antibodies.

We found several of the proteins to be expressed not only by urothelial cells but also by leukocytes, endothelial cells or histiocytes (Table 10, Fig. 10). Of the examined proteins only keratin 8 and ApoE were confined to urothelium; the other proteins were also present in other cell types. Based on the assumption that transcript and protein originates from the same cell, this clearly indicates that conclusions on the origin of the transcripts requires a histological examination, or other verification procedure. The amount of stroma in a biopsy, the vascularization (amount of endothelial cells), the level of leukocyte infiltration, and the grade of atypia of the urothelial cells were all parameters that seemed to influence the level of a given transcript.

The level of protein identified by immunostaining, disregarding the cell type expressing the protein, correlated well with the transcript level measured on the microarray (Fig. 10). However, no attempt was made to quantitate the immunostaining due to the often large heterogeneity in staining across the sections.

Proteins involved in posttranslational modification		9609	70	939	5099
Z23090_at	H sapiens mRNA for 28 kDa heat shock protein	1181	9689	5541	2883
S78522_at	Jarid3in carboxyl extension protein [human], "mRNA," 5' end	2522	2390	1894	1684
U12404_at	Human Csa-19 "mRNA," complete cds	1372	71	165	343
X54277_at	H sapiens CL 100 mRNA for protein tyrosine phosphatase	1727	1798	2284	1278
X52551_ma1_at	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)				
Cell membrane proteins		2387	1058	1191	2583
DD0017_at	Human lipocalin II mRNA	1423	1013	1244	1902
M33880_at	Human 26-kDa cell surface protein TAPA-1 "mRNA," complete cds				
Secreted proteins/hormones/growth factor related proteins		2774	3792	4130	6117
M17733_at	Human thymosin beta-4 "mRNA," complete cds				
Proteins related to immunology		4579	20	5638	9005
M83439_s_at	"Human Ig rearranged gamma chain "mRNA," V-J-C region and complete cds"	3684	2784	6031	2841
J00105_s_at	"Human beta-2 microglobulin gene "mRNA," 3' end"	3447	20	3373	11685
M57789_s_at	"Human (hybridoma H-210) anti-hepatitis A IgG variable "region," constant "region," complementation	3378	2880	1904	2591
M24194_at	Human MHC protein homologous to chicken B complex protein "mRNA," complete cds	2821	1098	1449	2367
D45824_s_at	Human HLA-B null allele mRNA	2780	429	2264	3206
X00274_at	Human gene for HLA-DR alpha heavy chain class II antigen (immune response gene) of the major	2360	1125	3442	3978
S82287_at	"beta 2-microglobulin (111b deleted between nucleotides 88-98) "human," colon cancer cell line "H	2235	137	1422	9736
M34516_at	Human omega light chain protein 14.1 (Ig lambda chain related) gene	1875	20	145	544
M94528_at	Human adipsin/complement factor D "mRNA," complete cds	1473	54	723	4064
S71043_ma1_s_at	Ig alpha 2-immunoglobulin A heavy chain subtype 2 (constant "region," germ line) "human," peripheral	1449	1184	1215	1058
M57710_at	Human IgE-binding protein (epsilon-BP) "mRNA," complete cds				
Nucleoproteins		3851	3351	2542	3234
M84711_at	Human v-fos transformation effector protein (Fos-1), "mRNA" complete cds	2812	6360	9363	1838
U42901_ma1_s_at	Human JF 10 (transin receptor precursor) 40 ribosome associated protein "gene," complete cds	2851	4333	5077	1310
D13413_ma1_s_at	Human mRNA for tumor-associated 120 kDa nuclear protein "p120," partial cds(carboxyl terminus)	2005	1873	1418	2290
K23405_at	Human homolog of rat insulinoma gene ("ig"), exon 6-158	1697	1853	3281	1581
M11353_at	Human H3.3 histone class C "mRNA," complete cds	1448	1117	1338	1175
M28813_at	Human nucleophosmin "mRNA," complete cds	1438	1139	1225	1493
J03827_at	Y box binding protein-1 (YB-1) mRNA				
Mitochondrial proteins		7848	3970	5895	5823
Z70759_at	H sapiens mitochondrial 16S rRNA gene (partial, 19-270759 nt) "mRNA"	1338	1550	1649	1405
X15341_at	Human COX VIa-L mRNA for cytochrome c oxidase liver-specific subunit VIa (EC 1.9.3.1)				
Other proteins		15733	1713	381	1298
M28311_s_at	Human cystic fibrosis antigen mRNA, complete cds	10368	20	20	20
M6757_s_at	ST60 Calcium binding protein A7	5344	64	104	162
L05187_at	"Homo sapiens small protein-rich protein 1 (SPRR1A) "gene," complete cds"	5389	20	39	310
L10343_at	Human elastin "gene," complete cds	3167	52	114	171
D84422_at	Human DRA for cystatin A	4856	8358	4730	3894
H03214-IT3391_at	Metalloproteinase 1	4930	20	20	319
M11006_at	Human migration inhibitory factor-related protein 2 (MIRP2) "gene," complete cds	4572	3636	3980	3168
X15064_at	Human mRNA for transcriptionally controlled tumor protein	4485	59	20	20
L05188_at	"Homo sapiens small protein-rich protein 2 (SPRR2B) "gene," complete cds"	4441	20	20	20
M18888_at	"Human small protein rich protein (Apo) "mRNA," clone 128"	4285	117	33	40
X53063_s_at	Human SPR2-1 gene for small protein rich protein (clone 12)	3885	3603	2730	1274
X55482_s_at	H sapiens THMT2 gene exon 11 (19-25452 nt) "mRNA" human DNA template-mRNA	3843	3170	2728	4056
H03549-IT3751_at	Wilm's Tumor-Related Protein	3809	20	20	20
M20030_s_at	"Human small protein rich protein (Apo) "mRNA," clone 130"	3490	20	20	20
X78223_s_at	H sapiens MAL gene exon 1 (end joined CDS).	1217	182	283	333
X06908_at	Human mRNA for lipocalin	3172	7843	8178	4858
M11147_at	Human keratin L chain "mRNA," complete cds	3031	20	52	384
M57348_s_at	H sapiens mRNA (clone 9712)	2805	1553	1408	2416
V05594_s_at	Human mRNA for metalloproteinase from cadmium-treated cells	2575	7538	6245	1892
U08155_s_at	Human chromosome 1q subtelomeric sequence 015553, 19-25553 nt "mRNA" human DNA template-CDS	2525	186	378	332
M54656_at	Human fatty acid binding protein homologue (FA-FABP) "mRNA," complete cds	2378	27	47	2971
Y07755_at	H sapiens S100A2 "gene," exon "1," 2 and 3	2156	3154	2439	1379
U78027_ma3_at	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-lye ribosomal pro	2101	1427	1223	1336
D38853_at	Human mRNA for calcitonin "complete cds"	1945	1342	2580	2932
X57351_s_at	Human 1-50 gene from interferon-inducible gene family	1819	2870	1179	825
M38581_at	Homo sapiens cellular ligand of interferon II (p11) "mRNA," complete cds	1771	2131	1619	1776
L20941_at	Human keratin heavy chain "mRNA," complete cds	1655	123	245	549
M57815_at	Human retinol acid-binding protein II (CRABP-II) gene	1652	79	66	62
X53299_s_at	H sapiens mRNA for IRAP	1525	20	20	451
X04470_s_at	Human mRNA for antileukoprotease (ALP) from cervix uterus	1472	1380	1439	1450
M57951_at	H sapiens mRNA for proliferation-associated gene (pag)	1416	213	360	149
H04059-IT4339_s_at	Homo sapiens Chemotactic Protein 1	1399	21	26	50
V07809_at	H sapiens mRNA for Progression Associated Protein	1311	325	557	911
J04152_ma1_s_at	M191 gene extracted from Human gastrin-releasing tumor-associated antigen GA733-1 protein "gene,"	1310	188	190	202
S81914_at	(EX-1) expression-inducible immediate-early gene "human," "interferon," "mRNA" "Partial," 1223 nt				

Expression of genes related to bladder wall

Gene name	Gene product	Bladder wall	Single cell solutions					Biopsies				
			Ta Gr1	Ta Gr1	Ta Gr1	T1 Gr1	T2 Gr1	Mean	T1 Gr1	T2 Gr1	T2 Gr1	Mean
Z19554_s_at	H.sapiens vimentin gene	1186	-	-	-	422	204	125	334	853	674	620
J02854_at	Human 20-kDa myosin light chain (MLC-2)	412	-	-	-	-	-	0	-	-	615	205
M21812_at	Human (clone PWHLC2-24) myosin light chain 2	175	-	433	-	-	690	225	374	427	410	404
U48959_at	Human myosin light chain kinase (MLCK)	621	-	-	-	-	-	-	-	-	617	206
X05276_at	Human mRNA for fibroblast tropomyosin TM30 (pl)	642	261	313	294	245	139	250	178	283	214	225
Z24727_at	H.sapiens tropomyosin isoform	464	55	76	98	56	59	69	365	468	607	480
M12125_at	"Human fibroblast muscle-type tropomyosin "	586	-	-	-	-	-	0	-	-	426	142
M19267_s_at	"Human tropomyosin "	284	-	90	-	207	-	59	482	313	188	334
M63391_rna1_at	Human desmin gene, complete cds.	392	-	192	-	-	-	38	-	-	905	302
M26576_cds2_at	Human alpha-1 collagen type IV gene, exon 52.	207	-	-	-	-	-	0	-	-	290	97
Sum of expressed units		4869	316	1104	392	930	1092	767	1743	2344	4956	3014
X74929_s_at	H.sapiens KRT8 mRNA for keratin 8	5006	2266	3494	2434	2450	3130	1296	2074	1423	390	1296

Table 2B

Table 3. Number of genes, out of 3400 genes examined, that are expressed as in the tumor-pool to which the tumor belongs, or altered as in a tumor pool of higher or lower stage or grade

Clinical data on tumor	5th superficial recurrence Grade II	First invasive tumor Grade III	Primary tumor, large solid muscle invasive Grade IV
Expression like tumor pool	770 genes	516 genes	625 genes
Unique to tumor	58	75	93
Increased expression similar to invasive Grade IV pool	24	47	-
Decreased expression similar to invasive Grade IV pool	19	22	-
Increased or decreased similar to Grade II		45	33

The lines in bold list genes that signal a higher stage or grade.

Table 4A Gene expression that signal a higher grade or stage

Gene Name	Gene product	Ts-01 Pool	Ta Single Tumor	T201V Pool	Deviation*	Bladder wall	20% Wall**	50% Wall
HG3147-H17217r_at	Mucin "3," intestinal (Gc:1653406)	0	330	541	On	0	0	0
HG860-H1880_at	Human mucin 6, gastric (single repeat clone)-human (fragment), partial CDS	0	426	493	On	0	0	0
V00787_s_at	Human mRNA for MDMPF (monocyte-derived neutrophil chemotactic factor)	0	327	393	On	224	44.9	112
B021300_f_at	Human unproductively rearranged Ig mu-chain mRNA V-region (VD), 8' end, clone mu-3A1A	0	284	219	On	0	0	0
X83482_at	Human mRNA for Fas/Apo-1 (clone pCRTM11-Fasdet(4,7))	0	236	367	On	0	0	0
X07690_at	Human mRNA for cytochrome 1b	323	0	0	Off	0	262.4	164
J06036_s_at	Human cathepsin E "mRNA," complete cds	1145	302	0	Decreased	0	918	872.6
B04424_at	Human cathepsin E (CTSE) gene	413	98	0	Decreased	0	330.4	206.6
U20794_s_at	Human transcription factor JunB (JunB) "gene," 5' region and complete cds	1250	324	0	Decreased	1060	1213.8	1169.5
X68768_at	Human PRAD1 mRNA for cyclin	438	0	0	Off	63	381.4	249.5
L35293_at	Human Cdc25 binding protein (CDBP1) "mRNA," complete cds	162	0	0	Off	0	129.6	61
S017083_s_at	Human prepro-neutrophil-like growth factor II (IGF-II) variant "mRNA," complete cds	1683	489	0	Decreased	0	1338.4	831.5
B062403_s_at	Human insulin-like growth factor binding protein 4 (IGFBP4) "mRNA," complete cds	998	245	0	Decreased	337	841.8	652.5
M34370_s_at	Homo sapiens (clone lambda MSP131) beta-microglobulin protein (MSP) gene	260	0	0	Off	0	224	140
U22170_s_at	Human prolactin secretory protein 57 "mRNA," complete cds	69	0	0	Off	0	71.2	44.5
U69263_at	Ap-1/22178 mRNA-RNA	116	0	0	Off	152	123.2	134
U72649_at	Human matrilin-2 precursor "mRNA," partial cds	888	274	289	Decreased	244	787.8	666
U81008_at	Human BTG2 (BTG2) "mRNA," complete cds	183	0	0	Off	76	168.6	134.5
U90816_at	Human p76 "mRNA," complete cds	250	0	0	Off	31	206.2	140.5
X63576_fm1_at	Human clone 23815 mRNA sequence	176	0	0	Off	0	140.8	68
X76180_at	Human gene for parvalbumin	263	0	0	Off	255	253.4	254
X07159_at	Human mRNA for lung anion chloride sensitive Na+ channel protein	188	0	0	Off	0	150.4	94
Y00264_at	Human mRNA for beta subunit of epithelial anion chloride-sensitive sodium channel	236	0	0	Off	183	272.8	238
Z76693_s_at	Human mRNA for amyloid AA precursor of Alzheimer's disease	196	0	0	Off	0	158.8	98
	Human mRNA for protein-tyrosine phosphatase NC-PTP/COM1							

Only genes scored as present are shown. *Deviation describes aberration from pool ** 20% and 50% describes expected units of expression if tumor pool was added 20% or 50% bladder wall components. Genes in bold do not need interrogation of bladder wall contribution. Off, genes that are turned off; On, genes that are turned on.

Table 4B Gene expression that signal a higher grade or stage

Gene Name	Gene Product	T2GIII Pool	2GIII Single tube	T2GIV Pool	Grade III po	Backdoor wall	20% Wt/WT	80% Wt/WT
X173501_at	H.sapiens gene for cytokereitin 20	0	162	162	On	0	0	0
X03689_s_at	Human mRNA fragment for elongation factor TU (N-terminals)	0	1845	2062	On	4233	846.6	2118.5
X04347_s_at	95p-X03689 Intype-RNA	0	1824	830	On	911	182.2	455.5
M21142_cds2_s_at	Human liver mRNA fragment DNA binding protein LPI homologous (C-terminus)	0	1100	839	On	782	160.4	301
J09106_s_at	guanine nucleotide-binding protein G-q-alpha-3 gene extracted from Human guanine nucleotide-binding protein alpha-subunit gene (G-q-alpha)	1137	9190	4802	Increased	3664	1642.4	2400.6
S82207_at	Human beta-2 microglobulin gene "mRNA," 3' end beta 2-microglobulin (115bp deleted between nucleotides 88-99) "Thuman," colon cancer cell line "HCT," mRNA "Mutant," 416 nt	619	4006	3909	Increased	2360	966.4	1489
M34616_at	Human omega light chain protein 14.1 (lg lambda chain related) gene	0	4080	6289	On	2235	447	1117.5
L02320_f_at	Human asplena (clones Hs lambda-17) lambda-like "gene," complete cds	0	373	734	On	0	0	0
M63438_s_at	Human Ig rearranged gamma chain "mRNA," V-J-C region and complete cds	0	1402	7075	On	4579	915.8	2289.5
M81700_s_at	Human (hybridoma H210) anti-hepatitis A IgG variable "region," constant "region," complementarity-determining regions "mRNA," complete cds	0	2420	4769	On	3447	685.4	1723.6
S71043_mna1_s_at	Ig alpha 2-murroglobulin A heavy chain subtype 2 constant "region," germ line "Thuman," peripheral blood "nautrophils," "Genomic," 1789 nt	0	1175	2608	On	1473	284.8	736.6
M14481_mna1_s_at	PTMA gene extracted from Human prothymosin alpha "mRNA," complete cds	0	1410	948	On	641	128.2	320.6
M18652_at	Human pancreatic elastase 1A mRNA, complete cds	0	466	222	On	201	40.2	190.6
M81832_s_at	Human 8-adenosylthymocysteine hydrolase (APCV) "mRNA," complete cds	0	233	128	On	71	14.2	36.6
M93484_at	Human set "gene," complete cds	0	294	213	On	169	31.8	79.6
X12871_mna1_at	hump at1 protein gene extracted from Human gene for heterogenous nuclear ribonucleoprotein (hnRNP) core protein A1	0	716	394	On	694	118.9	297
X16183_at	Human mRNA for 90-kDa heat-shock protein	880	1691	1790	Increased	919	652.6	782.6
Y08614_at	H.sapiens mRNA for CRU1 protein	0	171	136	On	72	14.4	30
Z49146_s_at	H.sapiens mRNA for ribosomal protein L20	616	2569	1801	Increased	2303	953.4	1459.5
Z48501_s_at	H.sapiens mRNA for polyadenylate binding protein II, IgB-Z48501 Intype-RNA	660	1893	2633	Increased	1263	760.6	911.6
HG3076-4T3238_s_at	Heterogeneous Nuclear Ribonucleoprotein "K," Alt. Splice 1	0	433	247	On	239	47.9	119.6
M36430_s_at	Human traneducin beta-1 subunit "mRNA," 3' end	0	608	266	On	118	23.6	69
HG417-4T417_s_at	Cathepsin B	0	2797	1763	On	1172	234.4	698
J02853_s_at	Human ADP/ATP carrier protein "mRNA," complete cds	0	301	408	On	337	67.4	168.6

J04040_a_at	Human calmodulin "mRNA," complete cds	0	425	348	On	0	0	0
M26311_a_at	Human cystic fibrosis antigen mRNA, complete cds	0	2359	1413	On	15733	3146.6	7086.5
X13546_fm1_at	Human HMG-17 gene for non-fibrona chromosomal protein HMG-17.	209	740	1126	Increased	222	210.8	215
X64220_at	Hsaaplens dcl mRNA	0	189	208	On	60	10	25
X07325_at	Hsaaplens p27 mRNA	0	363	693	On	0	0	0
L00205_at	Human Kib (epidermal "larin," type II) gene	80	0	0	Off	154	94.6	117
D10922_a_at	Human mRNA for PML-P-related receptor (H4693)	405	0	0	Off	20	401.2	266.5
D56643_a_at	Human spleen PAB1 (pseudautosomal boundary-like sequence) "mRNA," clone Sp2. Hsp-D56643 htype-mRNA	304	0	0	Off	0	291.2	182
L11672_at	Human Kruppel related zinc finger protein (KTF10) "mRNA," complete cds	2090	1770	1219	Decreased	370	3028	2030
B119370_at	Human spleen calbindin 27 gene, exon 1 and 2, and Alu repeat	305	0	0	Off	0	202	182.8
Z35402_fm1_o_at	Hsaaplens gene encoding "E-cadherin," exon 3 and joined CDS	782	230	242	Decreased	160	041.6	460.5
M26605_at	Human Haldin 2 (HIS2) mRNA, complete cds	210	0	0	Off	0	168	105
D06233_a_at	Human glutathione transferase class mu number 4 (GSTM4) "gene," complete cds	12810	0	0	Off	0	10014.4	8260
U31216_a_at	Human metabotropic glutamate receptor 1 alpha (mGluR1alpha) "mRNA," complete cds	317	0	0	Off	0	263.0	160.5
U33830_at	Human NF-kappa-B p50delta3 "mRNA," spliced transcript lacking exons 9 and "7," partial cds. Hsp-U33830 htype-mRNA	478	0	0	Off	67	353.0	287.5
U79293_at	Human clone 23901 mRNA sequence	164	0	0	Off	0	131.2	82
U79260_at	Human clone 23908 "mRNA," partial cds.	99	0	0	Off	0	78.2	49.5
X60703_a_at	Hsaaplens mRNA for SYT-65X, synovial sarcoma translocation junction	844	0	0	Off	0	676.2	422
X30646_at	Hsaaplens gene for G-HITc receptor	689	0	0	Off	124	676	406.5
X06800-H1680_at	Hsaaplens mRNA for ribbed kinase kinase 2 (human mucln 8, gastric (single repeat clone) -human (fragment), partial CDS	2080	881	604	Decreased	0	1678.2	1049.5
L08707_a_at	Human (clone L8) orphan G protein-coupled receptor "mRNA," complete cds	1793	0	493	Decreased	0	1434.4	896.5
R27740_f_at	Human immunoglobulin-related 14.1 protein "mRNA," complete cds	680	0	150	Decreased	109	493	340
R29335_at	Human hHC class II DO-alpha mRNA, partial cds	1110	0	0	Off	0	885.2	659.5
X68087_at	Hsaaplens a-myb mRNA	1043	0	217	Decreased	0	834.4	621.5
X05632_a_at	Hsaaplens mRNA for Arg protein tyrosine kinase-binding protein	281	0	0	Off	0	234.4	146.5
							208.8	130.5

Only genes scored as present are shown. *Deviation describes aberration from pool ** 20% and 50% describes expected units of expression if tumor pool was added 20% or 50% bladder wall components. Genes in bold do not need interrogation of bladder wall contribution. Off, genes that are turned off. On, genes that are turned on.

Table 5

Expression pattern				>=3 fold ch.	>=5 fold ch.	>=7 fold ch.	
N	↑	Ta	↑	T2-4	9 v	0	0
N	↑	Ta	→	T2-4	233 v	76	34
N	↑	Ta	↓	T2-4	164 v	51	23
N	→	Ta	↑	T2-4	612 v	262	141
N	→	Ta	→	T2-4	5407 v	6456	6768
N	→	Ta	↓	T2-4	264 v	92	41
N	↓	Ta	↑	T2-4	175 v	49	20
N	↓	Ta	→	T2-4	208 v	87	45
N	↓	Ta	↓	T2-4	2 v	0	0

Table 6

Connective tissue A													
Gene Name	Positi	Negati	Pairs	Pairs	U Pairs	I Pos	Fracti	Log Avg	PM E	MM E	Pos/Neg	Avg Difr	Abs Call
hum_alu_at	68	0	69	69	69	67	0.99	6.27	4	0	Inf	10744	P
L08499_at	19	0	20	20	20	18	0.95	7.03	3	0	Inf	6084	P
AFFX-HUMGAPDH/M33197_3_1	18	0	20	20	20	18	0.90	5.85	1	0	Inf	5588	P
L10343_at	19	0	20	20	20	18	0.95	6.38	2	0	Inf	5388	P
D23660_at	19	0	20	20	20	18	0.95	7.89	3	0	Inf	5345	P
AFFX-HSAC07/X00351_M_at	20	0	20	20	20	18	1.00	6.41	0	0	Inf	5185	P
D88422_at	18	0	20	20	20	18	0.90	7.09	5	0	Inf	5167	P
HG3214-HT3391_at	19	0	20	20	20	18	0.95	6.77	3	0	Inf	4966	P
M21005_at	10	3	20	20	20	18	0.50	1.87	0	0	3.3	4930	P
HG2873-HT3017_at	19	0	20	20	20	18	0.95	7.24	4	0	Inf	4372	P
HG3384-HT3541_at	19	0	20	20	20	18	0.95	7.09	4	0	Inf	4242	P
HG3549-HT3751_at	20	0	20	20	20	18	1.00	6.49	2	0	Inf	3843	P
M17885_at	20	0	20	20	20	18	1.00	6.88	2	0	Inf	3690	P
AFFX-HSAC07/X00351_5_at	17	0	20	20	20	18	0.85	5.46	0	0	Inf	3657	P
HG1800-HT1823_at	18	0	20	20	20	18	0.90	4.94	1	0	Inf	3582	P
M17886_at	17	1	20	20	20	18	0.85	4.70	0	0	17.0	3488	P
AFFX-HUMGAPDH/M33197_M_	18	0	20	20	20	18	0.90	5.29	0	0	Inf	3413	P
M18000_at	20	0	20	20	20	18	1.00	7.06	4	0	Inf	3315	P
M13934_cdn2_at	17	0	20	20	20	18	0.85	5.00	1	0	Inf	3281	P
AFFX-HSAC07/X00351_3_at	18	1	20	20	20	18	0.80	5.15	0	0	18.0	3211	P
M11147_at	17	0	20	20	20	18	0.85	6.32	2	0	Inf	3172	P
L08505_at	14	0	20	20	20	18	0.70	4.09	0	0	Inf	3024	P
AFFX-CreX-3_at	20	0	20	20	20	17	1.00	6.01	1	0	Inf	3008	P
M17793_at	18	1	20	20	20	18	0.90	6.09	1	0	18.0	2774	P
D78361_at	17	1	20	20	20	18	0.85	4.91	0	0	17.0	2518	P
L38941_at	20	0	20	20	20	18	1.00	6.50	1	0	Inf	2460	P
D00017_at	18	0	20	20	20	18	0.90	4.24	0	0	Inf	2387	P
AFFX-CreX-5_at	19	0	20	20	20	18	0.95	5.22	0	0	Inf	2382	P
L14530_at	18	0	20	20	20	18	0.85	6.56	2	0	Inf	2193	P
L14530-HT821_at	18	0	20	20	20	18	0.90	5.13	0	0	Inf	2159	P
D38583_at	17	2	20	20	20	18	0.85	4.82	0	0	8.5	2101	P
HG33-HT33_at	18	0	20	20	20	18	0.90	5.87	1	0	Inf	2077	P
L19527_at	19	0	20	20	20	18	0.95	4.69	1	0	Inf	1981	P
HG4319-HT4589_at	18	0	20	20	20	18	0.90	5.82	0	0	Inf	1960	P
AFFX-HUMGAPDH/M33197_5_1	17	0	20	20	20	17	0.85	5.57	2	0	Inf	1939	P
HG813-HT1613_at	13	1	20	20	20	17	0.90	5.59	1	0	Inf	1873	P
L20941_at	15	2	20	20	20	18	0.75	3.44	2	0	13.0	1771	P
M11353_at	15	2	20	20	20	18	1.00	5.61	4	0	7.5	1697	P
D79205_at	20	0	20	20	20	18	1.00	6.59	1	0	Inf	1639	P
AFFX-BioOn-3_at	12	2	20	20	20	17	0.60	2.53	0	0	6.0	1598	P
M21388_at	15	0	20	20	20	18	0.75	3.40	0	0	Inf	1572	P
D87735_at	17	0	20	20	20	18	0.85	4.85	1	0	Inf	1439	P
J03827_at	14	1	20	20	20	18	0.70	3.89	2	0	14.0	1409	P
HG384-HT384_at	12	0	20	20	20	18	0.60	4.02	3	0	Inf	1409	P
L11566_at	15	0	20	20	20	18	0.75	3.76	0	0	Inf	1399	P
HG4542 HT4947_at	12	1	20	20	20	18	0.60	4.06	0	0	12.0	1378	P
L26247_at	18	1	20	20	20	18	0.90	5.33	2	0	18.0	1375	P
D00854_at	19	0	20	20	20	18	0.95	4.77	0	0	Inf	1245	P

Slide 1

Connective tissue A

J00124_at	15	1	20	20	18.075	3.91	1	0	15.0	1210 P
D45370_at	14	1	20	20	17.070	2.56	0	0	14.0	1127 P
HG2279-HT2375_at	13	0	20	20	18.065	3.07	0	0	Inf	1112 P
M19283_at	17	2	20	20	18.085	3.74	2	1	8.5	1086 P
HG311-HT311_at	18	0	20	20	17.090	5.26	1	0	Inf	1067 P
M13903_at	13	0	20	20	18.065	2.57	0	0	Inf	1000 P
D14710_at	13	0	20	20	18.065	2.85	0	0	Inf	980 P
HG2708-HT2896_at	16	0	20	20	18.080	3.13	0	0	Inf	973 P
AC002115_cds1_at	11	0	20	20	18.055	2.71	0	0	Inf	941 P
D86429_at	12	0	20	20	18.060	3.21	0	0	Inf	917 P
J03592_at	16	0	20	20	18.080	3.50	0	0	Inf	905 P
D50840_at	19	0	20	20	18.095	5.59	4	0	Inf	851 P
D26068_at	16	1	20	20	18.080	3.30	0	1	16.0	821 P
J03181_at	18	1	20	20	18.090	4.33	0	0	18.0	799 P
HG1153-HT1163_at	9	0	20	20	18.045	2.17	0	0	Inf	772 P
L24203_at	13	2	20	20	18.065	3.15	1	0	6.5	762 P
D13746_at	11	0	20	20	17.055	2.04	0	0	Inf	744 P
M19483_at	13	0	20	20	18.065	3.28	0	0	Inf	683 P
D16217_at	12	0	20	20	18.050	2.35	0	0	Inf	681 P
M15681_at	14	0	20	20	18.070	3.49	0	0	Inf	653 P
HG987-HT987_at	13	2	20	20	18.085	3.18	1	0	6.5	640 P
D21261_at	7	0	20	20	18.035	1.71	0	0	Inf	623 P
AB001325_at	9	0	20	20	18.045	1.47	0	0	4.5	612 P
L19686_ma1_at	9	2	20	20	18.045	2.22	0	0	Inf	611 P
D13118_at	11	0	20	20	18.055	2.52	0	0	11.0	600 P
D29012_at	11	1	20	20	18.055	2.02	0	0	Inf	589 P
L09504_at	10	0	20	20	18.050	2.05	0	0	Inf	584 P
M14200_ma1_at	14	0	20	20	18.050	1.94	0	0	Inf	581 P
L08666_at	12	1	20	20	18.070	3.59	2	0	Inf	567 P
D31883_at	15	1	20	20	18.060	2.66	0	0	12.0	564 P
D16562_at	12	0	20	20	18.075	3.68	0	0	15.0	561 P
D88667_at	12	0	20	20	18.065	3.01	0	0	Inf	559 P
J04823_ma1_at	13	1	20	20	18.055	2.14	0	0	13.0	558 P
D85815_at	11	2	20	20	18.070	2.36	0	0	5.5	557 P
D11428_at	12	1	20	20	18.060	2.29	0	0	12.0	554 P
D26308_at	12	1	20	20	18.060	1.97	0	0	Inf	552 P
D26124_at	10	0	20	20	18.050	1.83	0	0	Inf	549 P
J01456_at	14	1	20	20	18.070	2.87	0	0	14.0	546 P
J04173_at	15	0	20	20	18.075	2.67	0	0	Inf	539 P
D87953_at	16	0	20	20	18.080	3.30	0	0	Inf	532 P
L16437_at	9	0	20	20	18.045	1.87	0	0	Inf	527 P
J04988_at	11	0	20	20	18.055	2.79	0	0	Inf	505 P
L38486_at	9	0	20	20	18.045	1.79	0	0	Inf	500 P
D87292_at	9	0	20	20	18.045	1.46	0	0	Inf	499 P
J02874_at	14	0	20	20	18.070	3.27	0	0	Inf	485 P
M19961_at	10	1	20	20	18.050	2.07	1	0	10.0	484 P
D00632_at	14	0	20	20	18.070	2.36	0	0	Inf	481 P
D38047_at	13	0	20	20	18.065	2.50	0	0	Inf	475 P
HG662-HT662_at	13	3	20	20	18.055	2.27	0	0	4.3	457 P
D14520_at	9	1	20	20	18.045	1.54	0	0	9.0	

Side 2

Connective tissue A										
K02765_at	13	1	20	20	18 0.85	1.66	0	0	0 13.0	455 P
AFFX-BioDn-5_at	11	1	20	20	18 0.55	1.60	0	0	0 11.0	450 P
HG174-HIT174_at	11	0	20	20	18 0.55	2.00	0	0	0 Inf	433 P
M16279_at	10	0	20	20	17 0.50	1.73	0	0	0 Inf	418 P
D23662_at	9	0	20	20	18 0.45	1.53	0	0	0 Inf	417 P
J02854_at	10	1	20	20	17 0.50	2.07	0	0	0 10.0	412 P
M18728_at	13	3	20	20	18 0.65	2.45	1	0	0 4.3	412 P
HG3494-HIT3688_at	8	1	20	20	17 0.40	1.35	0	0	0 8.0	410 P
J04080_at	13	1	20	20	18 0.65	3.09	0	0	0 13.0	407 P
D98548_at	7	0	20	20	18 0.35	1.52	0	0	0 Inf	404 P
D88479_at	8	0	20	20	18 0.40	1.57	0	0	0 Inf	404 P
D31846_at	8	1	20	20	18 0.40	1.35	0	0	0 8.0	402 P
D83874_at	8	0	20	20	18 0.45	2.26	0	0	0 Inf	398 P
D14812_at	8	0	20	20	18 0.45	1.51	0	0	0 Inf	396 P
J03040_at	8	0	20	20	18 0.40	2.06	0	0	0 Inf	393 P
AFFX-HSAC07X00361_3_at	12	0	20	20	17 0.60	2.80	0	0	0 Inf	392 P
L27843_at	8	0	20	20	17 0.40	1.47	0	0	0 4.3	391 P
D30655_at	13	3	20	20	18 0.65	3.06	0	0	0 4.3	391 P
J02902_at	7	1	20	20	18 0.35	1.95	0	0	0 7.0	391 P
L12168_at	10	0	20	20	18 0.50	2.54	0	0	0 Inf	390 P
L10284_at	14	0	20	20	18 0.70	3.39	0	0	0 Inf	388 P
D26598_at	10	1	20	20	18 0.50	1.87	0	0	0 10.0	387 P
L76200_at	11	1	20	20	18 0.55	1.89	0	0	0 11.0	384 P
J03459_at	8	3	20	20	18 0.45	1.81	1	0	0 3.0	381 P
D90209_at	14	0	20	20	17 0.70	3.34	0	0	0 Inf	380 P
D25274_at	14	2	20	20	17 0.70	2.26	0	0	0 7.0	378 P
D26598_at	10	0	20	20	18 0.50	1.86	0	0	0 Inf	359 P
L19605_at	10	0	20	20	17 0.50	1.66	0	0	0 Inf	338 P
AFFX-BioC-5_at	10	1	20	20	18 0.50	1.64	0	0	0 10.0	333 P
D78151_at	10	0	20	20	18 0.50	1.81	0	0	0 Inf	319 P
AJ000480_at	8	1	20	20	18 0.40	1.70	0	0	0 8.0	314 P
D23673_at	11	2	20	20	17 0.55	1.79	0	0	0 5.5	312 P
L11370_at	10	0	20	20	18 0.50	1.98	0	0	0 Inf	311 P
D00761_at	10	0	20	20	18 0.50	1.77	0	0	0 Inf	310 P
L49169_at	10	0	20	20	18 0.50	1.99	1	0	0 Inf	306 P
D83779_at	8	1	20	20	17 0.45	1.49	1	0	0 9.0	304 P
D28416_at	13	2	20	20	18 0.35	2.07	1	0	0 7.0	301 P
D25218_at	7	1	20	20	18 0.35	2.88	2	0	0 6.5	300 P
D45248_at	8	0	20	20	18 0.65	1.62	0	0	0 Inf	300 P
J04611_at	7	1	20	20	18 0.35	1.48	0	0	0 7.0	285 P
D63475_at	12	1	20	20	18 0.60	1.95	0	0	0 12.0	280 P
L13381_at	12	0	20	20	18 0.60	3.00	0	0	0 Inf	288 P
L25080_at	11	0	20	20	18 0.55	1.47	0	0	0 Inf	284 P
HG1862-HIT1897_at	10	2	20	20	18 0.50	1.72	0	0	0 5.0	281 P
AJ001421_at	7	0	20	20	18 0.35	1.05	0	0	0 Inf	276 P
K03195_at	14	1	20	20	18 0.70	3.33	3	0	0 14.0	274 P
L07633_at	12	1	20	20	17 0.60	2.38	0	0	0 12.0	270 P
D38048_at	10	0	20	20	18 0.50	2.40	0	0	0 Inf	264 P
L08246_at	10	2	20	20	18 0.50	1.76	1	0	0 5.0	260 P
AF005775_at	8	0	20	20	18 0.45	1.84	0	0	0 Inf	253 P

Side 3

Connective tissue A

D50310_at	9	1	20	20	18.045	1.79	0	0.9.0	247 P
HG1112-HT1112_at	11	1	20	20	18.055	1.83	0	0.11.0	244 P
L11285_at	9	2	20	20	18.045	1.67	0	0.4.5	244 P
D14689_at	8	2	20	20	18.040	1.35	0	0.4.0	242 P
D65654_at	10	1	20	20	18.050	2.28	0	0.10.0	242 P
D28423_at	9	1	20	20	17.045	2.26	0	0.8.0	241 P
D31765_at	8	1	20	20	18.040	2.07	1	0.8.0	240 P
HG2855-HT2995_at	8	2	20	20	18.040	1.95	0	0.4.0	240 P
M14058_at	10	1	20	20	18.050	2.37	0	0.10.0	240 P
D49400_at	9	2	20	20	17.045	1.66	1	1.4.5	239 P
D87258_at	8	1	20	20	18.040	1.48	0	0.8.0	238 P
D26128_at	7	0	20	20	17.035	1.17	0	0.1nf	237 P
L32977_at	13	1	20	20	18.065	2.73	0	0.13.0	237 P
D31767_at	8	2	20	20	17.040	1.33	0	0.4.0	236 P
D61380_at	10	2	20	20	18.050	1.67	0	0.5.0	231 P
D13988_at	10	0	20	20	18.035	1.33	0	0.1nf	228 P
AFFX-BioC-3_at	7	0	20	20	18.035	1.42	0	0.1nf	225 P
L76191_at	8	1	20	20	18.040	2.28	1	0.8.0	225 P
D42123_at	9	1	20	20	18.045	1.20	0	0.9.0	223 P
D11094_at	8	2	20	20	18.040	1.19	0	0.4.0	222 P
L25085_at	7	0	20	20	18.035	1.77	0	0.1nf	222 P
D29643_at	12	2	20	20	18.060	1.88	0	0.6.0	221 P
L11373_at	8	2	20	20	18.040	1.34	0	0.4.0	214 P
D17525_at	7	1	20	20	18.035	1.43	0	0.7.0	211 P
D21260_at	7	0	20	20	18.035	1.14	0	0.1nf	211 P
D28364_at	13	0	20	20	18.065	2.59	1	0.1nf	209 P
D63878_at	9	2	20	20	18.045	1.28	0	1.4.5	206 P
D78134_at	7	1	20	20	18.035	1.18	2	0.7.0	203 P
D38549_at	7	1	20	20	18.035	1.68	2	1.7.0	201 P
M14010_at	9	1	20	20	18.045	1.98	0	0.9.0	201 P
D21853_at	8	0	20	20	18.040	1.84	0	0.1nf	199 P
L40401_at	8	0	20	20	18.040	1.82	0	0.4.5	195 P
D63476_at	8	2	20	20	18.045	1.42	0	0.4.5	193 P
L40027_at	8	0	20	20	18.040	1.93	1	0.1nf	188 P
D00762_at	10	0	20	20	18.050	2.12	0	0.1nf	187 P
D17400_at	9	2	20	20	18.045	1.50	0	0.4.5	187 P
L03532_at	11	3	20	20	18.055	1.71	0	0.3.7	187 P
L08486_at	12	1	20	20	17.060	3.01	1	0.12.0	187 P
HG3995-HT4265_at	8	1	20	20	18.040	1.14	0	0.8.0	186 P
M11717_ma1_at	13	2	20	20	18.065	3.65	2	0.8.5	185 P
D13370_at	9	1	20	20	17.045	1.75	0	0.9.0	185 P
HG1116-HT1116_at	8	0	20	20	18.040	1.46	0	0.1nf	184 P
K03515_at	8	2	20	20	18.040	1.32	0	0.4.0	183 P
D17516_at	7	0	20	20	17.035	1.45	0	0.1nf	177 P
HG4272-HT4542_at	7	1	20	20	18.035	1.97	1	0.7.0	177 P
D28137_at	9	3	20	20	18.045	1.55	0	0.3.0	176 P
L22009_at	8	2	20	20	18.040	1.35	0	0.4.0	175 P
D44466_at	12	1	20	20	18.060	2.09	1	0.12.0	173 P
L29277_at	8	0	20	20	17.040	1.41	0	0.1nf	173 P
L00352_at	7	1	20	20	18.035	1.98	1	0.7.0	169 P

Side 4

Connective tissue A

L34587_at	7	1	20	20	18.035	1.46	0	0.7.0	168 P
L37042_at	9	0	20	20	18.045	1.42	0	0 Inf	168 P
D86955_at	8	2	20	20	18.040	1.35	0	0.4.0	168 P
D15050_at	11	0	20	20	17.055	1.77	0	0 Inf	166 P
L10838_at	8	0	20	20	18.040	1.16	0	0 Inf	166 P
D14043_at	10	1	20	20	18.050	1.73	0	0.10.0	159 P
D87071_at	8	2	20	20	17.040	1.12	0	0.4.0	157 P
D42043_at	11	2	20	20	18.055	2.07	0	0.5.5	155 P
L38932_at	9	0	20	20	18.045	1.29	0	0 Inf	152 P
D90276_at	9	1	20	20	18.045	1.85	1	0.8.0	148 P
M13450_at	13	3	20	20	18.065	2.36	0	0.4.3	148 P
M11726_at	9	2	20	20	18.045	1.35	0	0.4.5	147 P
L41690_at	9	2	20	20	18.045	1.90	0	0.4.5	146 P
D43950_at	7	0	20	20	18.035	1.52	0	0 Inf	145 P
D63851_at	8	2	20	20	18.040	1.12	0	0.4.0	143 P
L19314_at	7	0	20	20	17.035	1.64	0	0 Inf	143 P
L41668_ma1_at	8	0	20	20	17.040	1.87	0	0 Inf	142 P
D83004_at	9	1	20	20	17.045	1.89	0	1.9.0	141 P
K02574_at	9	1	20	20	18.045	1.80	1	0.8.0	138 P
M13782_at	10	2	20	20	18.050	2.18	0	0.5.0	138 P
HG2415-HT2511_at	10	2	20	20	18.050	1.29	0	0.5.0	135 P
L20773_at	8	2	20	20	18.040	1.39	0	1.4.0	134 P
D10923_at	8	1	20	20	18.040	1.66	0	0.8.0	132 P
M12759_at	10	2	20	20	18.050	1.70	1	0.5.0	131 P
M16038_at	7	0	20	20	18.035	1.77	0	0 Inf	131 P
D86963_at	8	1	20	20	18.040	1.52	0	0.8.0	128 P
J05248_at	10	0	20	20	17.050	2.28	0	0 Inf	128 P
D90084_at	7	1	20	20	18.035	1.11	0	0.7.0	124 P
AF007875_at	8	1	20	20	18.040	1.33	0	0.8.0	123 P
D00726_at	7	0	20	20	18.035	1.62	0	0 Inf	123 P
J05243_at	7	0	20	20	18.045	1.82	0	0 Inf	122 P
L13761_ma1_at	7	0	20	20	18.035	1.52	0	0 Inf	119 P
L38951_at	10	0	20	20	18.050	1.86	0	0 Inf	119 P
M18533_at	12	2	20	20	18.060	3.76	4	0.6.0	119 P
J04605_at	7	1	20	20	18.035	1.22	0	0.7.0	117 P
D38553_at	7	2	20	20	18.035	1.48	0	0 Inf	116 P
L36531_at	7	0	20	20	18.035	1.46	1	0.3.5	116 P
L14837_at	9	2	20	20	18.045	2.20	2	0.4.5	113 P
HG4102-HT4372_at	7	1	20	20	18.035	1.12	0	0.7.0	109 P
L40395_at	8	2	20	20	18.040	1.38	0	0.4.0	107 P
D30756_at	8	1	20	20	18.040	2.08	2	0.8.0	106 P
L47738_at	8	0	20	20	17.040	0.90	0	0 Inf	105 P
D13641_at	9	3	20	20	18.045	1.05	0	0.8.0	104 P
D45399_at	9	3	20	20	18.045	1.85	0	0.3.0	104 P
L27706_at	12	2	20	20	18.060	1.93	0	0.6.0	104 P
D50683_at	9	3	20	20	18.045	1.47	0	0.3.0	100 P
HG2167-HT2237_at	9	1	20	20	18.045	1.19	0	0.9.0	99 P
D29641_at	7	1	20	20	18.035	1.43	0	0.7.0	98 P
L13977_at	7	1	20	20	18.035	1.58	1	0.7.0	97 P
L34600_at	7	0	20	20	18.035	1.05	0	0 Inf	95 P

Side 5

	Connective tissue A										
D42053_at	8	1	20	20	18 0.40	1.47	0	0.80	94 P		
M14123_xp12_at	9	3	20	20	18 0.45	1.36	1	0.30	93 P		
D14638_at	7	1	20	20	18 0.35	0.92	0	0.70	92 P		
L27841_at	8	1	20	20	18 0.40	1.00	0	0.40	-92 P		
AF010193_at	7	1	20	20	18 0.35	1.07	0	0.70	91 P		
D50926_at	11	2	20	20	18 0.55	1.24	0	0.55	90 P		
M11321_at	10	1	20	20	18 0.50	1.35	0	0.100	90 P		
HG1102-HT1102_at	7	1	20	20	18 0.35	1.68	1	0.70	89 P		
L40393_at	12	2	20	20	17 0.60	2.43	0	0.60	89 P		
D90003_at	9	1	20	20	18 0.45	1.59	1	0.90	86 P		
M14219_at	10	1	20	20	18 0.50	1.99	1	0.100	86 P		
M14536_at	7	0	20	20	18 0.35	0.98	0	0. Inf	85 P		
M13695_at	9	3	20	20	18 0.45	2.24	1	0.30	85 P		
L19711_at	8	0	20	20	18 0.40	1.67	0	0. Inf	84 P		
L76703_at	9	2	20	20	18 0.45	2.08	1	0.45	84 P		
O63390_at	10	1	20	20	18 0.50	2.52	2	0.100	82 P		
HG831-HT031_at	9	2	20	20	18 0.45	1.31	1	0.45	78 P		
D21255_at	9	1	20	20	18 0.45	1.93	1	0.90	77 P		
D76129_at	9	3	20	20	18 0.45	1.60	1	0.30	77 P		
L48513_at	13	3	20	20	18 0.65	1.87	1	1.43	77 P		
M14636_at	9	3	20	20	18 0.45	1.62	1	2.30	73 P		
M15796_at	7	2	20	20	18 0.35	1.66	0	0.35	73 P		
HG1103-HT1103_at	9	2	20	20	18 0.45	1.51	1	0.45	71 P		
L35240_at	7	1	20	20	18 0.35	1.02	0	0.70	67 P		
L77886_at	9	3	20	20	17 0.45	2.27	2	0.30	59 P		
D14659_at	9	3	20	20	18 0.45	1.81	1	0.30	54 P		
J04156_at	8	2	20	20	18 0.40	1.23	1	0.40	54 P		
D87457_at	7	2	20	20	18 0.40	2.72	4	0.40	48 P		
L20321_at	8	1	20	20	18 0.35	0.92	1	0.70	32 P		
L20814_at	9	3	20	20	18 0.45	1.61	1	1.30	28 P		

Connective tissue B											
Gene Nam	Positive	Negative	Pairs	Pairs Usd	InAv Pos	Fractl Log	Avg	PM Exces:MM	Exces Pos/Neg	Avg Diff	Abs Call
hum_alu_a	69	0	69	69	67	1.00	7.19	12	0 Inf	12502 P	
U46692_m	19	0	20	20	18	0.95	7.15	3	0 Inf	10030 P	
AFEX-HUN	18	0	20	20	18	0.90	6.06	0	0 Inf	5799 P	
AFEX-HSA	20	0	20	20	18	1.00	6.50	0	0 Inf	5422 P	
U14969_at	20	0	20	20	18	1.00	6.79	0	0 Inf	4539 P	
M60854_at	19	1	20	20	18	0.95	6.50	2	0 19.0	4473 P	
AFEX-Cre	18	0	20	20	18	0.95	7.67	3	0 Inf	4430 P	
M81757_at	18	0	20	20	18	0.90	6.62	2	0 Inf	4389 P	
U14973_at	19	0	20	20	18	0.95	6.06	1	0 Inf	4281 P	
AFEX-HSA	19	0	20	20	18	0.95	6.11	1	0 Inf	4114 P	
U14970_at	18	0	20	20	18	0.95	6.15	2	0 Inf	3928 P	
U14968_at	18	0	20	20	18	0.90	7.18	3	0 Inf	3885 P	
U14972_at	17	0	20	20	18	0.85	5.60	2	0 Inf	3695 P	
M84711_at	17	1	20	20	18	0.85	7.59	5	1 17.0	3651 P	
AFEX-HUN	17	0	20	20	18	0.85	5.08	0	0 Inf	3483 P	
M24194_at	19	0	20	20	18	0.95	5.89	0	0 Inf	3378 P	
U12465_at	19	0	20	20	18	0.95	6.01	0	0 Inf	3327 P	
M64716_at	17	2	20	20	18	0.85	5.15	3	0 8.5	3228 P	
S79522_at	19	0	20	20	18	0.95	6.42	4	0 Inf	3161 P	
AFEX-Cre	19	0	20	20	18	0.95	6.86	1	0 Inf	2966 P	
AFEX-HSA	18	0	20	20	17	0.90	5.87	0	0 Inf	2793 P	
AFEX-HUN	17	0	20	20	18	0.85	5.95	4	0 Inf	2690 P	
U14971_at	18	0	20	20	18	0.90	5.27	1	0 Inf	2645 P	
M77232_at	20	0	20	20	18	1.00	7.99	6	0 Inf	2618 P	
M94856_at	18	0	20	20	18	0.90	8.28	10	0 Inf	2525 P	
U12404_at	20	0	20	20	18	1.00	6.77	2	0 Inf	2506 P	
U09953_at	18	1	20	20	18	0.90	6.29	3	0 18.0	2488 P	
M32053_at	20	0	20	20	18	1.00	6.29	1	0 15.0	2129 P	
U58682_at	15	1	20	20	17	0.75	4.14	2	0 Inf	2053 P	
U49069_m	18	0	20	20	18	0.90	5.83	2	0 Inf	2005 P	
M32405_at	13	2	20	20	17	0.65	3.40	1	0 6.5	1876 P	
M31520_at	20	0	20	20	18	1.00	6.23	4	0 Inf	1875 P	
M84526_at	14	1	20	20	18	0.70	3.38	0	0 14.0	1819 P	
M38591_at	19	0	20	20	18	0.95	6.10	3	0 Inf	1735 P	
M95787_at	17	0	20	20	18	0.85	4.53	1	0 Inf	1655 P	
M97815_at	17	0	20	20	18	0.85	4.05	0	0 Inf	1653 P	
M86400_at	18	0	20	20	18	0.90	5.75	3	0 Inf	1565 P	
AFEX-BicL	15	2	20	20	17	0.80	3.26	0	0 8.0	1506 P	
M26880_at	16	0	20	20	18	0.80	7.17	9	0 Inf	1489 P	
M63138_at	12	1	20	20	18	0.60	2.92	0	0 12.0	1489 P	
M57710_at	18	1	20	20	18	0.90	6.45	2	1 18.0	1449 P	
M23613_at	17	1	20	20	18	0.85	5.57	4	0 17.0	1448 P	
M33680_at	15	0	20	20	18	0.75	3.69	1	0 Inf	1423 P	
M27891_at	14	0	20	20	18	0.70	3.55	0	0 Inf	1363 P	
S81914_at	18	0	20	20	18	0.80	5.75	1	0 Inf	1310 P	
U25789_at	16	0	20	20	18	0.80	5.97	2	0 Inf	1265 P	
M74542_at	14	1	20	20	18	0.70	3.88	0	0 14.0	1233 P	
M36690_at	15	1	20	20	18	0.75	3.97	0	0 15.0	1172 P	
S66738_at	16	1	20	20	18	0.80	5.75	0	0 15.0	1151 P	
M34182_at	7	2	20	20	18	0.35	1.43	0	0 3.5	924 P	

Side 1

Connective tissue B																			
302934_al	16	1	20	20	18.080	4.82	0	0	0	0	0	0	0	0	0	0	0	0	0
33379_al	16	0	20	20	18.080	3.59	0	0	0	0	0	0	0	0	0	0	0	0	0
M50047_al	17	0	20	20	18.085	4.42	1	1	1	1	1	1	1	1	1	1	1	1	1
U17077_al	15	0	20	20	18.075	3.94	0	0	0	0	0	0	0	0	0	0	0	0	0
M76378_al	13	0	20	20	18.065	4.01	0	0	0	0	0	0	0	0	0	0	0	0	0
M93056_al	14	0	20	20	18.070	4.58	1	1	1	1	1	1	1	1	1	1	1	1	1
U15008_al	15	0	20	20	17.075	3.48	0	0	0	0	0	0	0	0	0	0	0	0	0
M64332_al	12	1	20	20	18.060	2.32	0	0	0	0	0	0	0	0	0	0	0	0	0
M69043_al	14	1	20	20	18.070	4.12	2	2	2	2	2	2	2	2	2	2	2	2	2
U32944_al	15	1	20	20	17.075	4.21	0	0	0	0	0	0	0	0	0	0	0	0	0
M55593_al	12	1	20	20	18.060	2.46	0	0	0	0	0	0	0	0	0	0	0	0	0
U09813_al	15	0	20	20	18.075	4.39	0	0	0	0	0	0	0	0	0	0	0	0	0
M98447_al	10	0	20	20	18.050	2.31	0	0	0	0	0	0	0	0	0	0	0	0	0
U41635_al	13	0	20	20	18.065	1.97	0	0	0	0	0	0	0	0	0	0	0	0	0
U51478_al	15	1	20	20	18.075	4.38	0	0	0	0	0	0	0	0	0	0	0	0	0
M66849_al	13	1	20	20	18.065	4.24	1	1	1	1	1	1	1	1	1	1	1	1	1
U04313_al	14	0	20	20	18.070	3.59	0	0	0	0	0	0	0	0	0	0	0	0	0
U48959_al	14	1	20	20	18.070	3.07	1	1	1	1	1	1	1	1	1	1	1	1	1
U46751_al	13	1	20	20	18.065	3.61	0	0	0	0	0	0	0	0	0	0	0	0	0
S77356_al	12	2	20	20	18.060	3.32	1	1	1	1	1	1	1	1	1	1	1	1	1
M23254_al	15	1	20	20	18.075	1.35	0	0	0	0	0	0	0	0	0	0	0	0	0
U44839_al	9	2	20	20	18.065	3.06	0	0	0	0	0	0	0	0	0	0	0	0	0
M62982_al	13	2	20	20	18.060	0.98	0	0	0	0	0	0	0	0	0	0	0	0	0
M88466_al	8	2	20	20	18.045	3.45	2	2	2	2	2	2	2	2	2	2	2	2	2
U21128_al	11	3	20	20	18.055	2.95	0	0	0	0	0	0	0	0	0	0	0	0	0
U50523_al	12	2	20	20	18.060	2.64	0	0	0	0	0	0	0	0	0	0	0	0	0
U30255_al	11	0	20	20	17.055	2.54	0	0	0	0	0	0	0	0	0	0	0	0	0
M60858_al	16	0	20	20	18.080	3.50	1	1	1	1	1	1	1	1	1	1	1	1	1
U37690_al	10	0	20	20	18.050	2.08	0	0	0	0	0	0	0	0	0	0	0	0	0
S45630_al	11	0	20	20	18.055	1.96	0	0	0	0	0	0	0	0	0	0	0	0	0
M98539_al	13	2	20	20	18.065	2.84	0	0	0	0	0	0	0	0	0	0	0	0	0
S75463_al	10	1	20	20	18.050	1.71	0	0	0	0	0	0	0	0	0	0	0	0	0
M28540_al	15	2	20	20	18.075	3.66	0	0	0	0	0	0	0	0	0	0	0	0	0
M80563_al	13	0	20	20	18.065	2.43	0	0	0	0	0	0	0	0	0	0	0	0	0
M22538_al	13	0	20	20	18.065	2.32	0	0	0	0	0	0	0	0	0	0	0	0	0
M75126_al	11	0	20	20	18.055	2.14	0	0	0	0	0	0	0	0	0	0	0	0	0
U56637_al	12	0	20	20	18.060	2.95	0	0	0	0	0	0	0	0	0	0	0	0	0
U46499_al	14	1	20	20	17.070	3.14	0	0	0	0	0	0	0	0	0	0	0	0	0
U12779_al	7	0	20	20	18.035	1.00	0	0	0	0	0	0	0	0	0	0	0	0	0
U51004_al	13	1	20	20	18.065	2.57	0	0	0	0	0	0	0	0	0	0	0	0	0
U11881_al	8	1	20	20	18.040	1.49	0	0	0	0	0	0	0	0	0	0	0	0	0
U03057_al	12	0	20	20	17.060	2.03	0	0	0	0	0	0	0	0	0	0	0	0	0
M96739_al	7	1	20	20	18.035	1.37	0	0	0	0	0	0	0	0	0	0	0	0	0
M22760_al	13	0	20	20	18.065	3.54	0	0	0	0	0	0	0	0	0	0	0	0	0
U62962_al	8	0	20	20	18.040	1.65	0	0	0	0	0	0	0	0	0	0	0	0	0
AFFX-BioC	12	2	20	20	18.060	1.72	0	0	0	0	0	0	0	0	0	0	0	0	0
S73591_al	13	2	20	20	18.065	2.35	0	0	0	0	0	0	0	0	0	0	0	0	0
M65391_al	8	1	20	20	18.040	1.61	0	0	0	0	0	0	0	0	0	0	0	0	0
M88338_al	11	2	20	20	18.055	1.48	0	0	0	0	0	0	0	0	0	0	0	0	0
M76482_al	14	3	20	20	18.070	2.79	0	0	0	0	0	0	0	0	0	0	0	0	0
M22382_al	13	0	20	20	18.065	2.58	0	0	0	0	0	0	0	0	0	0	0	0	0
M22490_al	8	1	20	20	18.040	1.47	0	0	0	0	0	0	0	0	0	0	0	0	0

Side 2

Connective tissue B

M57567_al	9	1	20	20	18.045	1.77	0	0.9.0	377 P
U15932_al	14	1	20	20	18.070	3.10	0	1.14.0	375 P
AFFX-HSA	12	0	20	20	17.060	2.29	0	0 Inf	374 P
S74017_al	15	2	20	20	18.075	2.72	0	0.7.5	372 P
M74491_al	12	0	20	20	18.060	2.09	0	0 Inf	363 P
U37519_al	11	1	20	20	18.055	2.22	0	0.11.0	368 P
U29084_al	15	1	20	20	18.075	3.61	1	1.15.0	353 P
U62402_al	9	0	20	20	18.045	1.99	0	0 Inf	350 P
U29953_m	12	0	20	20	18.060	2.67	0	0 Inf	349 P
U46025_al	11	0	20	20	18.055	1.97	0	0 Inf	349 P
U46570_al	9	1	20	20	18.045	1.53	0	0.9.0	347 P
S73149_al	8	0	20	20	18.040	1.20	0	0 Inf	346 P
U33821_al	10	1	20	20	18.050	1.94	0	0.10.0	346 P
U09117_al	8	2	20	20	18.040	1.33	0	0.4.0	344 P
AFFX-BhoC	15	2	20	20	18.075	2.38	0	0.7.5	340 P
M37104_al	17	0	20	20	18.085	3.43	2	0 Inf	338 P
M59815_al	10	2	20	20	17.050	2.14	0	0.5.0	337 P
M75099_al	9	1	20	20	18.045	1.69	0	0.9.0	331 P
U07857_al	17	1	20	20	17.055	3.44	0	0.17.0	330 P
M28209_al	13	0	20	20	18.065	2.74	0	0 Inf	321 P
U02020_al	15	2	20	20	18.075	3.40	0	0.7.5	315 P
M31525_al	10	3	20	20	18.050	1.92	0	0.3.3	314 P
M60278_al	9	2	20	20	18.045	2.06	0	0.4.5	308 P
M83751_al	13	0	20	20	18.065	2.21	0	0 Inf	307 P
M63167_al	10	1	20	20	17.050	1.51	0	0.10.0	306 P
U15085_al	13	0	20	20	18.065	2.34	0	0 Inf	306 P
M55621_al	12	0	20	20	17.060	2.65	0	0 Inf	304 P
S72487_al	8	0	20	20	18.040	1.71	0	0 Inf	301 P
U00968_al	10	0	20	20	18.050	1.12	0	0 Inf	301 P
M94630_al	9	2	20	20	18.045	1.31	1	0.4.5	290 P
M59465_al	11	2	20	20	18.055	2.68	2	0.5.5	289 P
M37583_al	13	1	20	20	18.065	3.67	1	0.13.0	288 P
M84349_al	11	1	20	20	17.055	2.58	0	0.11.0	286 P
M99701_al	13	1	20	20	18.065	2.72	1	0.13.0	282 P
U37122_al	10	1	20	20	17.050	1.95	1	0.10.0	282 P
U57342_al	7	0	20	20	18.035	1.06	0	0 Inf	281 P
M34079_al	9	3	20	20	17.045	1.53	0	0.3.0	280 P
S68616_al	8	2	20	20	18.040	1.35	0	0.4.0	279 P
M69096_al	14	2	20	20	17.070	3.20	0	0.7.0	276 P
M88279_al	11	0	20	20	18.055	2.06	0	0 Inf	276 P
M31013_al	12	2	20	20	18.060	2.13	0	0.6.0	274 P
M84345_al	11	1	20	20	18.055	1.77	0	0.11.0	274 P
U37689_al	8	0	20	20	18.040	1.35	0	0 Inf	269 P
U41515_al	11	1	20	20	18.055	2.31	0	0.11.0	269 P
M37984_al	8	2	20	20	18.060	1.43	0	0.4.0	267 P
M89458_al	12	0	20	20	18.055	1.93	0	0 Inf	265 P
U02570_al	11	1	20	20	18.045	2.28	1	0.11.0	263 P
M68864_al	9	1	20	20	18.055	2.10	0	0.9.0	260 P
M31984_al	11	1	20	20	18.045	2.60	0	0.11.0	257 P
M35678_al	10	2	20	20	18.050	1.55	0	1.5.0	255 P
U62015_al	8	0	20	20	18.040	1.58	0	0 Inf	253 P
U44755_al	7	1	20	20	18.035	1.45	0	0.7.0	250 P

Side 3

Connective tissue B									
M80244_al	9	1	20	20	17.045	1.50	0	0.9.0	249 P
U02493_al	9	1	20	20	18.045	2.04	0	0.8.0	247 P
M29696_al	8	1	20	20	18.040	1.21	0	0.8.0	246 P
M73720_al	12	0	20	20	17.060	2.59	0	0.1nf	246 P
U09579_at	9	2	20	20	18.045	2.07	1	0.4.5	242 P
M92303_al	7	2	20	20	18.035	1.41	0	0.3.5	240 P
U20285_al	7	1	20	20	18.035	1.80	0	0.7.0	240 P
U50733_al	9	1	20	20	18.045	1.83	0	0.9.0	239 P
M29536_al	13	2	20	20	18.065	2.11	0	0.6.5	238 P
M63483_al	11	3	20	20	18.055	1.75	0	0.3.7	238 P
M83186_al	10	3	20	20	18.050	1.87	0	0.3.3	238 P
U40391_m	9	1	20	20	18.045	1.50	0	0.9.0	237 P
M86667_al	13	0	20	20	18.065	3.08	1	0.1nf	233 P
SS3911_al	11	2	20	20	17.055	1.84	0	0.5.5	233 P
AFFX-BioC	10	1	20	20	18.050	1.81	0	0.10.0	232 P
M33308_al	13	0	20	20	18.065	3.20	1	0.1nf	231 P
S83364_al	9	1	20	20	18.045	2.20	0	0.9.0	231 P
U06863_at	7	0	20	20	18.035	1.14	0	0.1nf	230 P
M37033_al	11	3	20	20	18.055	1.97	1	0.3.7	229 P
U21931_at	9	2	20	20	18.045	1.55	0	0.4.5	229 P
M36341_al	13	1	20	20	17.065	2.63	0	0.13.0	225 P
M55040_al	8	2	20	20	18.040	1.18	0	0.4.0	225 P
M80254_al	8	1	20	20	18.040	1.69	0	0.8.0	223 P
M57763_al	7	2	20	20	18.035	1.35	0	0.3.5	222 P
M83088_al	8	2	20	20	18.040	1.71	0	0.4.0	221 P
M33336_al	16	1	20	20	18.080	2.70	0	0.16.0	217 P
M58028_at	9	1	20	20	18.045	1.46	0	0.8.0	213 P
M63573_at	11	2	20	20	18.055	2.70	0	0.5.5	213 P
U63541_al	11	2	20	20	18.055	1.87	0	0.5.5	213 P
U24105_al	9	0	20	20	18.045	1.86	0	0.1nf	212 P
M64992_at	10	1	20	20	17.050	2.15	1	0.10.0	210 P
U38846_al	12	1	20	20	18.060	1.89	0	0.12.0	209 P
U40282_al	11	3	20	20	18.055	1.59	0	0.3.7	208 P
M26576_c	7	2	20	20	18.035	1.40	0	0.3.5	207 P
S77812_at	9	2	20	20	18.045	1.80	0	0.4.5	206 P
U30825_at	10	2	20	20	17.050	2.18	0	0.5.0	206 P
M33552_al	9	1	20	20	18.045	1.19	0	0.8.0	205 P
U52112_m	9	1	20	20	18.045	1.97	1	0.9.0	205 P
M56603_at	12	2	20	20	17.060	2.77	2	0.6.0	202 P
S82240_at	12	1	20	20	18.060	3.55	2	0.12.0	201 P
M86528_at	7	1	20	20	18.035	1.20	0	0.7.0	200 P
M22632_al	9	1	20	20	18.045	1.38	0	0.9.0	199 P
M81601_al	11	2	20	20	18.055	1.77	0	0.5.5	199 P
M94556_al	12	1	20	20	18.080	2.15	0	0.12.0	199 P
M37435_al	7	1	20	20	18.035	1.74	0	0.7.0	197 P
M64098_at	11	2	20	20	18.055	2.31	0	0.5.5	197 P
U20998_at	8	2	20	20	18.040	2.68	1	0.4.0	196 P
U36764_al	14	1	20	20	17.070	3.29	0	0.14.0	196 P
U12255_al	8	1	20	20	18.040	1.73	0	0.8.0	195 P
U54778_at	8	1	20	20	18.040	1.23	0	0.8.0	195 P
M69039_al	14	2	20	20	17.070	2.86	0	0.7.0	194 P
M24802_at	11	0	20	20	18.055	2.34	0	0.1nf	193 P

Slide 4

Connective tissue B																			
U52100_al	12	0	20	20	18 0.60	2.09	0	0 Inf	192 P										
U03100_al	12	3	20	20	18 0.60	2.40	0	0 4.0	189 P										
M64347_al	10	2	20	20	18 0.50	1.08	0	0 5.0	186 P										
M81780_c	7	0	20	20	18 0.35	1.01	0	0 Inf	186 P										
M29877_al	10	1	20	20	18 0.50	1.51	0	1 10.0	181 P										
M62831_al	9	0	20	20	18 0.45	1.63	0	0 Inf	180 P										
U49785_al	12	2	20	20	18 0.60	1.76	1	0 Inf	178 P										
M31627_al	12	2	20	20	18 0.60	1.96	0	0 6.0	177 P										
U07424_al	10	3	20	20	18 0.50	1.50	0	0 3.3	177 P										
M89473_al	8	2	20	20	18 0.50	1.03	0	0 4.0	174 P										
U52101_al	7	1	20	20	18 0.35	1.22	0	0 7.0	174 P										
U16127_al	8	2	20	20	18 0.40	1.73	0	0 4.0	173 P										
U03698_al	10	2	20	20	18 0.60	2.96	0	0 5.0	172 P										
U57877_al	8	2	20	20	18 0.40	1.10	0	0 4.0	169 P										
M23114_al	14	1	20	20	17 0.70	2.87	1	0 14.0	167 P										
M73547_al	10	3	20	20	18 0.50	1.38	0	0 3.3	165 P										
U21049_al	7	0	20	20	18 0.35	0.95	0	0 Inf	165 P										
S67325_al	8	1	20	20	18 0.40	1.24	0	0 8.0	163 P										
U18009_al	10	2	20	20	18 0.50	1.86	0	0 5.0	163 P										
U50330_al	8	1	20	20	18 0.40	1.22	0	0 8.0	163 P										
U51878_al	12	2	20	20	18 0.60	1.84	0	0 6.0	160 P										
U24166_al	12	1	20	20	18 0.60	2.02	0	0 12.0	158 P										
U34962_al	10	2	20	20	18 0.50	1.26	0	0 5.0	152 P										
M57399_al	9	3	20	20	18 0.45	1.33	0	0 3.0	150 P										
U53476_al	7	1	20	20	18 0.35	1.13	0	0 7.0	150 P										
M24470_al	8	1	20	20	17 0.40	1.20	0	0 8.0	148 P										
M29927_al	8	0	20	20	17 0.40	1.33	0	0 Inf	147 P										
U51711_al	9	1	20	20	17 0.45	1.67	0	0 9.0	146 P										
M34057_al	10	3	20	20	18 0.50	2.37	1	0 3.3	145 P										
U43286_al	10	1	20	20	18 0.50	1.61	0	1 3.3	143 P										
U53445_al	14	3	20	20	17 0.70	3.30	1	0 14.0	143 P										
S65583_rn	9	1	20	20	18 0.45	1.46	1	0 3.0	141 P										
M86546_al	10	1	20	20	18 0.50	1.83	1	0 10.0	140 P										
U31384_al	9	1	20	20	17 0.50	1.49	0	0 9.0	139 P										
M63175_al	8	2	20	20	18 0.45	1.48	0	0 4.0	138 P										
M93283_al	10	2	20	20	18 0.40	1.48	0	0 5.0	138 P										
U30888_al	8	2	20	20	17 0.50	1.39	0	0 4.0	138 P										
U47101_al	9	0	20	20	18 0.40	1.54	0	0 Inf	138 P										
M97287_al	8	2	20	20	18 0.45	1.92	0	2 4.0	137 P										
AFEX-M27	9	0	20	20	18 0.40	1.29	1	0 Inf	136 P										
U51240_al	7	1	20	20	18 0.45	2.11	0	0 7.0	136 P										
U49070_al	8	0	20	20	18 0.35	1.11	0	0 Inf	135 P										
M33195_al	9	1	20	20	18 0.40	1.08	0	0 9.0	133 P										
M58830_al	11	3	20	20	18 0.45	1.29	0	0 3.7	133 P										
U07802_al	10	2	20	20	18 0.55	1.45	1	0 5.0	133 P										
U39317_al	7	2	20	20	17 0.50	1.85	0	0 3.5	132 P										
U61374_al	9	1	20	20	18 0.35	2.00	1	0 9.0	132 P										
M88776_r	9	1	20	20	18 0.45	1.43	0	0 9.0	130 P										
M22877_al	14	1	20	20	18 0.45	1.12	0	0 14.0	129 P										
M91036_r	7	1	20	20	17 0.70	2.26	1	0 7.0	128 P										
S77763_al	9	2	20	20	18 0.35	0.88	0	0 4.5	126 P										
U58334_al	7	0	20	20	18 0.45	1.34	0	0 Inf	125 P										

Side 5

Connective tissue B																			
M64929_at	10	1	20	20	18 0.50	2.14	1	0	10.0	124 P									
S72008_at	10	0	20	20	17 0.50	2.43	1	0	Inf	124 P									
M35416_at	9	3	20	20	18 0.45	1.39	0	0	3.0	122 P									
M37721_at	12	3	20	20	18 0.60	2.38	1	0	4.0	122 P									
M55671_at	8	1	20	20	18 0.40	1.97	1	0	8.0	122 P									
M27492_at	8	1	20	20	18 0.45	1.71	1	0	9.0	121 P									
U52969_at	7	1	20	20	18 0.35	1.15	0	0	7.0	118 P									
M55642_at	13	2	20	20	18 0.65	3.06	3	0	6.5	117 P									
S81419_at	8	1	20	20	18 0.40	1.23	0	0	8.0	117 P									
U01147_at	8	1	20	20	18 0.40	1.42	0	0	8.0	116 P									
U10439_at	8	1	20	20	18 0.40	1.89	0	0	8.0	116 P									
M59916_at	8	2	20	20	18 0.40	1.19	0	0	4.0	115 P									
U24152_at	8	2	20	20	18 0.40	1.26	0	0	4.0	115 P									
M74524_at	7	0	20	20	18 0.35	2.07	1	0	Inf	114 P									
M83738_at	8	2	20	20	18 0.40	1.98	1	0	4.0	114 P									
S43646_at	7	2	20	20	18 0.35	1.31	0	0	3.5	114 P									
U0952_at	9	2	20	20	18 0.45	1.64	1	0	4.5	114 P									
U09770_at	8	1	20	20	17 0.40	1.08	0	0	8.0	114 P									
U15782_at	7	1	20	20	18 0.35	1.68	0	0	7.0	113 P									
U40368_at	9	1	20	20	18 0.45	1.88	1	0	8.0	113 P									
M23197_at	9	0	20	20	18 0.45	1.35	0	0	Inf	111 P									
U14193_at	8	2	20	20	17 0.40	1.13	0	0	4.0	109 P									
U37510_at	7	2	20	20	18 0.35	1.69	0	0	3.5	109 P									
U02082_at	11	0	20	20	18 0.55	1.54	0	0	Inf	108 P									
U47742_at	9	2	20	20	18 0.45	1.57	1	0	4.5	108 P									
J50553_at	8	0	20	20	18 0.40	1.20	0	0	Inf	106 P									
U25171_at	9	1	20	20	18 0.45	2.12	0	0	8.0	104 P									
M63603_at	10	2	20	20	17 0.40	1.16	0	0	8.0	103 P									
U07358_at	9	2	20	20	18 0.50	1.51	0	0	1.50	103 P									
U16031_at	9	3	20	20	18 0.45	1.51	1	0	4.5	103 P									
S83366_at	9	2	20	20	18 0.45	1.50	0	0	3.0	103 P									
M80482_at	7	1	20	20	18 0.45	1.78	0	0	4.5	101 P									
M96803_at	7	1	20	20	18 0.35	1.34	0	0	7.0	100 P									
S77415_at	9	2	20	20	18 0.45	1.49	1	0	7.0	99 P									
S71018_at	8	0	20	20	18 0.45	2.53	2	0	4.5	95 P									
U13695_at	11	0	20	20	18 0.40	1.47	0	0	Inf	95 P									
U39400_at	10	3	20	20	18 0.35	1.12	0	0	Inf	95 P									
M77698_at	9	3	20	20	18 0.55	2.52	0	0	3.3	94 P									
U37251_at	10	1	20	20	18 0.50	1.81	1	0	3.0	92 P									
M90696_at	10	2	20	20	18 0.45	2.32	1	0	10.0	91 P									
U28386_at	9	3	20	20	18 0.50	1.61	1	0	5.0	89 P									
S67156_at	8	0	20	20	18 0.45	1.71	3	1	3.0	88 P									
U28686_at	9	0	20	20	18 0.45	2.73	2	0	Inf	86 P									
U35046_at	10	1	20	20	18 0.40	1.84	0	0	Inf	85 P									
M30269_at	7	2	20	20	17 0.50	1.70	1	0	1.90	83 P									
M34309_at	9	3	20	20	18 0.35	2.17	2	0	10.0	82 P									
M37197_at	10	2	20	20	18 0.45	2.00	1	0	3.5	82 P									
U45976_at	11	1	20	20	18 0.45	1.72	0	0	3.0	82 P									
S80562_at	9	2	20	20	18 0.50	1.80	0	0	5.0	80 P									
					18 0.55	2.70	0	0	11.0	77 P									
					18 0.45	2.06	1	0	1.45										

Side 6

Connective tissue B

U33818_al	9	1	20	20	18 0.45	0.99	0	1 9.0	77 P
M22995_al	9	0	20	20	18 0.45	1.52	0	0 Inf	76 P
U14747_al	8	2	20	20	18 0.40	1.09	0	0.40	76 P
M81118_al	9	3	20	20	18 0.45	1.52	2	1.30	75 P
M28983_al	7	2	20	20	18 0.35	1.30	1	0.35	74 P
M65217_al	7	3	20	20	18 0.45	2.24	2	0.30	72 P
M37825_al	10	3	20	20	18 0.50	1.50	0	0.33	70 P
M54992_al	10	3	20	20	18 0.50	1.38	0	0.33	70 P
U10117_al	9	3	20	20	18 0.45	1.52	1	0.30	70 P
U12471_al	7	2	20	20	18 0.35	1.55	0	0.35	70 P
U18242_al	9	2	20	20	18 0.45	2.09	0	0.45	70 P
U26032_al	9	3	20	20	18 0.45	1.63	1	0.30	70 P
M32886_al	10	2	20	20	17 0.50	0.94	0	0.50	66 P
U18291_al	9	2	20	20	18 0.45	2.26	1	0.45	66 P
S76965_al	8	2	20	20	18 0.40	1.70	2	0.40	65 P
U23070_al	9	3	20	20	18 0.45	1.44	2	0.30	65 P
M81378_al	7	1	20	20	18 0.35	1.05	0	0.70	63 P
U49436_al	10	2	20	20	18 0.50	2.41	2	0.50	63 P
M25393_al	9	3	20	20	18 0.45	1.61	1	1.30	62 P
M86679_al	9	3	20	20	18 0.45	1.74	2	0.30	62 P
M62397_al	9	2	20	20	18 0.45	1.92	1	0.45	60 P
M63623_al	7	2	20	20	18 0.35	1.40	0	0.35	57 P
U23942_al	7	0	20	20	18 0.35	1.40	0	0 Inf	56 P
U18062_al	8	1	20	20	18 0.40	1.83	1	0.80	50 P
S67788_al	8	2	20	20	18 0.40	1.33	0	0.40	49 P
M74093_al	8	2	20	20	18 0.40	1.09	0	0.40	48 P
U00951_al	8	2	20	20	18 0.40	1.61	1	0.40	47 P
U50939_al	7	2	20	20	18 0.35	1.47	1	0.35	46 P
U24576_al	8	2	20	20	18 0.40	2.15	1	0.40	42 P
U07151_al	8	2	20	20	18 0.40	1.14	0	0.40	40 P
U38810_al	8	1	20	20	18 0.40	1.37	1	0.80	40 P
U13948_al	9	2	20	20	18 0.45	1.61	1	0.45	37 P
S78569_al	7	1	20	20	18 0.35	0.89	0	0.70	35 P
U28833_al	7	1	20	20	18 0.35	1.04	0	1.70	33 P
U29615_al	8	2	20	20	18 0.40	1.05	0	0.40	33 P
M81882_al	8	2	20	20	18 0.40	1.65	1	0.40	31 P
U57452_al	7	1	20	20	18 0.35	0.96	0	0.70	28 P

Gene Name	Connective tissue C													Avg Diff	Abs Call
	Posit	Negat	Pain	Pain	Pos	Fractl	Log Avg	PM	Ex	MM	Excess	Pos/Neg			
Z23090_at	20	0	20	20	18	1.00	6.28	1	0	Inf	0	Inf	9609 P		
Z70759_at	20	0	20	20	18	1.00	8.75	11	0	Inf	0	Inf	7648 P		
Z12952_at	18	0	20	20	18	0.90	6.95	3	0	Inf	0	Inf	7468 P		
X07695_at	20	0	20	20	18	1.00	6.77	2	0	Inf	0	Inf	7458 P		
hum_aliu_at	69	0	69	68	67	1.00	7.07	11	0	Inf	0	Inf	7071 P		
X69150_at	19	0	20	20	18	0.95	7.89	8	0	Inf	0	Inf	8256 P		
X17206_at	20	0	20	20	18	1.00	7.81	8	0	Inf	0	Inf	4828 P		
X16084_at	19	0	20	20	18	0.95	8.14	6	0	Inf	0	Inf	4572 P		
X56932_at	20	0	20	20	18	1.00	7.69	5	0	Inf	0	Inf	4210 P		
AFFX-HUMGAPDH/M33197_3_at	20	0	20	20	18	1.00	7.15	2	0	Inf	0	Inf	4188 P		
AFFX-HSAC07/X00351_M_at	20	0	20	20	18	1.00	6.52	1	0	Inf	0	Inf	3970 P		
X08022_at	19	0	20	20	18	0.95	6.50	1	0	Inf	0	Inf	3963 P		
X03342_at	20	0	20	20	18	1.00	7.76	5	0	Inf	0	Inf	3818 P		
X67247_ma1_at	20	0	20	20	18	1.00	8.34	6	0	Inf	0	Inf	3725 P		
X08617_at	20	0	20	20	18	1.00	6.38	2	0	Inf	0	Inf	3387 P		
X15940_at	19	0	20	20	18	0.95	7.29	5	0	Inf	0	Inf	3375 P		
X63527_at	19	0	20	20	18	0.95	7.71	7	0	Inf	0	Inf	3282 P		
X05908_at	19	0	20	20	18	0.95	8.70	8	0	Inf	0	Inf	3217 P		
AFFX-CreX-3_at	19	0	20	20	18	0.95	8.12	6	0	Inf	0	Inf	3155 P		
AFFX-HSAC07/X00351_3_at	20	0	20	20	18	1.00	6.57	2	0	Inf	0	Inf	2894 P		
X73460_at	19	0	20	20	18	0.95	6.62	3	0	Inf	0	Inf	2949 P		
X62691_at	20	0	20	20	18	1.00	7.33	4	0	Inf	0	Inf	2885 P		
AFFX-HSAC07/X00351_5_at	19	0	20	20	18	0.95	6.46	1	0	Inf	0	Inf	2782 P		
X00274_at	20	0	20	20	18	1.00	7.97	8	0	Inf	0	Inf	2780 P		
AFFX-HUMGAPDH/M33197_M_at	18	0	20	20	18	0.90	5.92	0	0	Inf	0	Inf	2639 P		
X79234_at	20	0	20	20	18	1.00	8.10	4	0	Inf	0	Inf	2602 P		
X55954_at	20	0	20	20	18	1.00	7.53	6	0	Inf	0	Inf	2495 P		
Z26876_at	20	0	20	20	18	0.85	7.65	6	0	Inf	0	Inf	2490 P		
Z28407_at	17	0	20	20	18	0.85	5.59	1	0	Inf	0	Inf	2386 P		
Y07755_at	19	0	20	20	18	0.95	7.10	2	0	Inf	0	Inf	2378 P		
X64707_at	19	0	20	20	18	0.95	5.87	2	0	Inf	0	Inf	2268 P		
AFFX-CreX-5_at	19	0	20	20	18	0.95	7.77	3	0	Inf	0	Inf	2185 P		
U78027_ma3_at	18	2	20	20	18	0.90	7.38	6	0	Inf	0	Inf	2156 P		
X67683_at	18	0	20	20	18	0.95	5.62	1	0	Inf	0	Inf	2126 P		
AFFX-HUMGAPDH/M33197_5_at	18	0	20	20	18	0.95	7.18	6	0	Inf	0	Inf	2120 P		
X69391_at	18	0	20	20	18	0.95	7.24	4	0	Inf	0	Inf	2094 P		
AB002533_at	18	0	20	20	18	0.90	5.92	0	0	Inf	0	Inf	2063 P		
X68277_at	19	0	20	20	18	0.95	8.28	7	0	Inf	0	Inf	1972 P		
X53777_at	18	1	20	20	18	0.80	7.13	6	0	Inf	0	Inf	1915 P		
X55715_at	20	0	20	20	18	1.00	7.32	2	0	Inf	0	Inf	1744 P		
X52851_ma1_at	20	0	20	20	18	1.00	6.55	3	0	Inf	0	Inf	1727 P		
X67951_at	20	0	20	20	18	1.00	6.97	2	0	Inf	0	Inf	1472 P		
X77584_at	19	0	20	20	18	0.95	7.09	3	0	Inf	0	Inf	1470 P		
X02152_at	18	0	20	20	18	0.90	6.78	2	0	Inf	0	Inf	1432 P		
X57959_at	19	0	20	20	18	0.95	7.24	3	0	Inf	0	Inf	1426 P		
X13839_at	18	0	20	20	18	0.90	6.81	3	0	Inf	0	Inf	1405 P		
AFFX-BioDr-3_at	17	2	20	20	18	0.85	4.13	0	0	Inf	0	Inf	1401 P		
X52066_at	17	1	20	20	18	0.85	6.56	5	0	Inf	0	Inf	1361 P		
X15341_at	20	0	20	20	18	1.00	6.91	6	0	Inf	0	Inf	1338 P		
X56997_ma1_at	17	0	20	20	18	0.85	5.20	2	0	Inf	0	Inf	1308 P		

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JL

Connective tissue C									
X60908_at	18	0	20	20	18 0.90	7.15	4	0	Inf
X60489_at	18	0	20	20	18 0.95	6.91	4	0	Inf
X12447_at	15	0	20	20	18 0.75	3.29	1	0	Inf
Z25749_ma1_at	18	1	20	20	18 0.90	5.26	0	0	18.0
X51466_at	18	0	20	20	18 0.80	5.14	1	0	Inf
X53331_at	18	0	20	20	18 0.90	6.29	1	0	Inf
Z19574_ma1_at	18	0	20	20	18 0.95	5.04	0	0	Inf
X82593_at	19	0	20	20	18 0.95	4.56	0	0	Inf
X95404_at	15	0	20	20	18 0.75	4.66	1	0	Inf
AF001548_ma1_at	17	0	20	20	18 0.85	5.12	1	0	Inf
X15183_at	17	1	20	20	18 0.85	6.82	2	0	17.0
U94586_at	20	0	20	20	17 1.00	8.01	6	0	Inf
X16560_at	17	0	20	20	18 0.85	6.16	3	0	Inf
U65932_at	19	0	20	20	18 0.95	5.61	0	0	Inf
X07686_at	17	0	20	20	18 0.85	5.88	1	0	Inf
X15822_at	18	0	20	20	18 0.90	5.08	3	0	Inf
V00572_at	20	0	20	20	18 1.00	6.57	2	0	Inf
X04412_at	17	1	20	20	18 0.85	4.49	1	0	17.0
X93036_at	16	0	20	20	17 0.80	4.59	0	0	Inf
Y00433_at	17	0	20	20	18 0.85	4.30	1	0	Inf
X65614_at	18	0	20	20	18 0.90	5.02	1	0	Inf
U90815_at	16	1	20	20	18 0.90	5.53	3	0	18.0
X16832_at	16	0	20	20	18 0.80	4.30	0	0	Inf
X05276_at	19	0	20	20	18 0.95	4.58	0	0	Inf
AFFX-HSAC07/X00351_3_at	18	0	20	20	18 0.90	4.98	0	0	Inf
U73824_at	18	0	20	20	18 0.95	6.59	3	0	Inf
V01612_ma1_at	19	0	20	20	18 0.95	6.39	2	0	Inf
U93205_at	18	0	20	20	18 0.90	3.74	0	0	Inf
X13238_at	17	1	20	20	18 0.85	5.69	1	0	17.0
X56494_at	14	1	20	20	18 0.70	3.58	1	0	14.0
X07979_at	18	1	20	20	17 0.90	5.96	2	0	18.0
X86693_at	16	0	20	20	18 0.80	5.33	2	0	Inf
Z48950_at	17	0	20	20	18 0.85	4.43	0	0	Inf
X02317_at	18	0	20	20	18 0.95	5.45	0	0	Inf
X59634_at	17	1	20	20	18 0.85	5.44	0	0	17.0
Z24727_at	17	0	20	20	18 0.85	5.17	2	0	Inf
X56468_at	18	0	20	20	18 0.90	5.18	1	0	Inf
X03100_cd4s2_at	14	0	20	20	18 0.70	3.39	1	0	Inf
Y00503_at	18	0	20	20	18 0.80	4.44	0	0	Inf
U67171_at	12	0	20	20	18 0.60	2.64	0	0	Inf
U78095_at	16	1	20	20	17 0.80	3.28	0	0	16.0
X15880_at	10	1	20	20	18 0.50	3.08	0	0	10.0
X69550_at	13	1	20	20	18 0.65	2.30	0	0	13.0
X62654_ma1_at	17	1	20	20	17 0.85	3.73	1	0	17.0
X57698_at	17	0	20	20	18 0.85	3.49	0	0	Inf
U72511_at	15	0	20	20	18 0.75	3.49	1	0	Inf
X04108_at	13	2	20	20	18 0.65	2.50	0	0	6.5
X58314_at	14	0	20	20	18 0.70	3.09	0	0	Inf
X51521_at	17	1	20	20	18 0.95	4.60	1	0	19.0
X60036_at	18	0	20	20	18 0.85	4.60	0	0	Inf
U78284_at	15	1	20	20	18 0.75	3.95	2	0	15.0
X59892_at	12	1	20	20	18 0.60	2.57	0	0	12.0

Connective tissue C																			
U70370_at	12	2	20	20	18.060	2.66	1	0.60	361 P										
X91504_at	11	1	20	20	18.055	1.54	0	0.11.0	360 P										
U73843_at	13	1	20	20	18.085	3.39	1	0.13.0	356 P										
L20888_at	13	0	20	20	18.065	2.63	0	0 Inf	356 P										
X16662_at	14	2	20	20	18.070	3.64	1	0.7.0	355 P										
X54304_at	15	0	20	20	18.075	3.90	0	0 Inf	350 P										
Y00764_at	17	1	20	20	18.085	5.54	2	0.17.0	347 P										
Z29505_at	18	0	20	20	18.090	4.62	0	0 Inf	345 P										
U90878_at	16	1	20	20	18.080	5.35	0	0.16.0	335 P										
Z21507_at	15	1	20	20	18.075	4.28	0	0.15.0	335 P										
Z32765_at	11	1	20	20	18.055	2.00	0	0.11.0	330 P										
X60221_at	17	1	20	20	18.085	6.00	0	0.17.0	329 P										
X62320_at	10	0	20	20	18.050	2.31	0	0 Inf	327 P										
X83218_at	17	0	20	20	18.085	5.28	0	0 Inf	322 P										
X52003_at	9	2	20	20	18.045	2.33	0	0.4.5	321 P										
X15882_at	11	2	20	20	18.055	1.84	0	0.5.5	314 P										
X17042_at	16	0	20	20	17.080	5.83	3	0 Inf	314 P										
X78136_at	15	1	20	20	18.075	4.66	0	0.15.0	309 P										
Y00486_rna1_at	8	0	20	20	18.040	1.74	0	0 Inf	307 P										
X13794_rna1_at	16	1	20	20	18.080	4.91	1	0.16.0	300 P										
U70735_at	17	0	20	20	18.085	3.67	0	0 Inf	288 P										
X71973_at	12	1	20	20	18.060	2.30	0	0.12.0	287 P										
U78521_at	8	0	20	20	18.045	1.26	0	0 Inf	296 P										
U94855_at	18	0	20	20	18.090	4.74	0	0 Inf	293 P										
D29805_at	11	3	20	20	18.055	2.57	1	0.3.7	291 P										
X75851_at	16	1	20	20	18.080	4.65	1	0.16.0	290 P										
AFFX-BioDn-5_at	13	0	20	20	18.065	3.14	0	0 Inf	288 P										
U77604_at	13	0	20	20	18.085	2.79	0	0.13.0	286 P										
X90858_at	15	2	20	20	18.075	3.54	0	0.7.5	285 P										
X86809_at	11	1	20	20	18.055	1.89	0	0.11.0	283 P										
X80692_at	14	0	20	20	18.070	3.84	0	0 Inf	276 P										
U72512_at	7	0	20	20	17.035	1.41	0	0 Inf	272 P										
X55733_at	14	0	20	20	18.070	3.92	0	0 Inf	272 P										
Y00281_at	14	2	20	20	18.070	3.22	0	0.7.0	272 P										
U80313_at	17	0	20	20	18.085	3.78	0	0 Inf	270 P										
X81817_at	15	2	20	20	18.075	3.43	1	0.7.5	266 P										
Z48199_at	10	1	20	20	18.050	1.74	0	0.10.0	263 P										
U77504_at	10	0	20	20	18.050	2.03	0	0 Inf	262 P										
X75593_at	10	2	20	20	18.050	2.92	1	0.5.0	260 P										
Z14244_at	18	0	20	20	17.090	6.43	5	0 Inf	260 P										
X91247_at	11	1	20	20	18.055	2.03	1	0.18.0	258 P										
X08885_at	11	1	20	20	18.060	2.72	0	0.11.0	257 P										
X76180_at	12	1	20	20	18.050	2.26	0	0.12.0	255 P										
X76717_at	10	1	20	20	18.055	1.75	0	0.10.0	251 P										
U65785_at	11	0	20	20	18.065	3.06	0	0 Inf	249 P										
X91257_at	13	0	20	20	18.065	4.72	0	0 Inf	249 P										
X87838_at	16	0	20	20	18.080	3.02	1	0.12.0	248 P										
X75252_at	12	1	20	20	18.060	2.12	0	0.12.0	247 P										
X97074_at	12	0	20	20	18.060	3.23	0	0 Inf	242 P										
X16135_at	14	2	20	20	18.070	1.72	0	0.7.0	242 P										
X99688_at	8	1	20	20	18.045	1.72	0	0.9.0	242 P										
U34569_at	13	2	20	20	17.065	1.94	0	0.6.5	241 P										

Side 3

Connective tissue C									
X13444_at	9	0	20	20	18.045	1.61	0	0 Inf	241 P
U70732_ma1_at	9	2	20	20	18.045	1.35	0	0 4.5	240 P
X71428_at	11	1	20	20	18.055	2.25	0	0 11.0	240 P
U83115_at	13	0	20	20	18.065	3.05	1	0 Inf	239 P
X82434_at	11	0	20	20	18.055	1.84	0	0 Inf	237 P
X59417_at	14	2	20	20	18.070	2.91	1	1 7.0	231 P
X57346_at	13	1	20	20	17.065	3.80	0	0 13.0	230 P
X85765_ma1_at	9	0	20	20	18.045	1.61	0	0 Inf	229 P
X13546_ma1_at	15	0	20	20	17.075	2.97	0	0 Inf	222 P
X52730_ma1_at	8	0	20	20	18.040	1.24	0	0 Inf	222 P
X74104_at	15	1	20	20	18.075	4.00	1	0 15.0	222 P
U66878_at	9	2	20	20	17.045	2.00	0	0 4.5	221 P
Z27113_at	11	1	20	20	18.055	2.14	0	0 11.0	221 P
U66059_cde7_at	10	1	20	20	18.050	1.73	0	0 10.0	220 P
D13146_cds1_at	7	0	20	20	18.035	1.70	0	0 Inf	218 P
AFFX-Bloc-5_at	16	0	20	20	18.080	3.02	0	0 Inf	217 P
X69910_at	15	1	20	20	18.075	3.67	0	0 15.0	217 P
U78678_at	9	1	20	20	18.045	1.58	0	0 9.0	215 P
X76013_at	11	1	20	20	18.055	2.70	0	0 11.0	215 P
U70867_at	9	1	20	20	18.045	1.44	0	0 9.0	212 P
X69433_at	9	1	20	20	18.035	1.37	0	0 7.0	212 P
X69924_ma1_at	7	1	20	20	18.045	1.98	1	0 Inf	208 P
U77827_at	8	0	20	20	18.045	2.00	1	0 4.5	209 P
X69908_ma1_at	9	2	20	20	18.045	2.00	1	0 4.5	208 P
X80200_at	10	1	20	20	17.050	2.04	0	0 10.0	208 P
Z11793_at	15	1	20	20	18.075	4.49	4	0 15.0	208 P
U81556_at	12	2	20	20	18.060	2.25	0	0 6.0	207 P
U67963_at	9	1	20	20	18.045	2.10	0	0 9.0	206 P
X88585_at	14	1	20	20	18.070	4.48	1	0 14.0	206 P
U68566_at	10	2	20	20	18.050	1.94	0	0 5.0	204 P
U77396_at	8	0	20	20	18.040	1.53	0	0 Inf	201 P
U88629_at	12	1	20	20	18.060	3.30	0	0 12.0	199 P
X02612_at	12	1	20	20	18.080	2.99	0	0 12.0	199 P
X15187_at	14	1	20	20	18.070	3.68	0	0 14.0	188 P
Y00282_at	14	0	20	20	18.070	3.70	1	0 Inf	199 P
U65611_at	11	1	20	20	18.055	2.16	0	0 11.0	192 P
X72964_at	12	0	20	20	18.060	2.74	0	0 Inf	192 P
U73379_at	12	0	20	20	17.060	1.94	0	0 Inf	191 P
X56253_ma1_at	12	1	20	20	18.080	2.65	1	0 12.0	191 P
X64559_at	10	1	20	20	18.050	1.50	0	0 10.0	190 P
U86529_at	7	0	20	20	18.035	1.56	0	0 Inf	189 P
X04368_at	11	1	20	20	18.055	2.47	0	0 11.0	188 P
X52947_at	14	0	20	20	18.070	5.43	2	0 Inf	188 P
U70663_at	6	0	20	20	18.040	1.58	0	0 Inf	187 P
X89750_at	18	0	20	20	18.085	4.23	0	0 Inf	186 P
Y08976_at	9	1	20	20	18.045	1.58	0	0 9.0	185 P
X69689_at	7	0	20	20	18.035	1.59	0	0 Inf	183 P
X01388_at	7	1	20	20	18.035	1.02	0	0 7.0	182 P
U70063_at	9	3	20	20	18.045	2.13	0	0 3.0	176 P
U72517_at	10	2	20	20	18.050	1.56	0	0 5.0	175 P
X76228_at	11	1	20	20	18.055	2.50	0	0 11.0	175 P
X78549_at	13	0	20	20	17.065	1.73	1	0 Inf	175 P

Connective tissue C									
	7	0	20	20	18 0.35	1.05	0	0 Inf	174 P
Z14000_at	13	1	20	20	18 0.65	4.22	0	0 13.0	165 P
U79254_at	9	0	20	20	18 0.45	1.84	0	0 Inf	165 P
X62078_at	10	3	20	20	18 0.50	1.40	0	0 3.3	163 P
U94585_at	11	1	20	20	18 0.55	1.50	0	0 11.0	162 P
U72066_at	9	1	20	20	18 0.45	2.60	0	0 9.0	161 P
U88964_at	9	1	20	20	18 0.45	1.35	0	0 9.0	160 P
U70660_at	16	0	20	20	17 0.80	3.99	2	0 Inf	160 P
X52541_at	16	0	20	20	18 0.80	3.20	0	0 Inf	160 P
X95586_at	10	1	20	20	17 0.50	1.89	1	0 10.0	159 P
X71129_at	8	0	20	20	18 0.40	1.65	0	0 Inf	158 P
X53416_at	8	0	20	20	18 0.40	1.58	0	0 8.0	157 P
X12794_at	8	1	20	20	18 0.40	1.58	0	0 8.0	157 P
X61970_at	13	0	20	20	18 0.65	3.44	0	0 Inf	157 P
Z37986_at	9	1	20	20	18 0.45	1.81	0	0 9.0	157 P
J04182_at	12	1	20	20	18 0.60	2.60	0	0 12.0	157 P
AFFX-BioC-3_at	11	1	20	20	18 0.55	2.12	0	0 11.0	156 P
X14787_at	12	2	20	20	18 0.60	4.02	0	1 6.0	155 P
X62535_at	10	0	20	20	18 0.50	2.78	1	0 Inf	155 P
X85373_at	11	0	20	20	18 0.55	2.75	1	0 Inf	155 P
X98484_at	10	1	20	20	18 0.50	1.71	0	0 10.0	154 P
X98311_at	9	0	20	20	18 0.45	1.80	0	0 Inf	154 P
L00205_at	12	0	20	20	18 0.60	2.47	0	0 Inf	154 P
X16316_at	10	2	20	20	18 0.50	1.87	0	0 5.0	153 P
U69263_at	14	1	20	20	17 0.70	2.22	0	0 14.0	152 P
X74801_at	11	0	20	20	18 0.55	3.34	0	0 Inf	152 P
U70322_at	13	1	20	20	18 0.65	2.19	0	0 13.0	151 P
D86988_at	7	0	20	20	18 0.35	1.09	0	0 Inf	151 P
V00563_at	11	1	20	20	18 0.55	2.59	1	0 11.0	150 P
X76029_at	7	2	20	20	18 0.35	1.35	0	0 3.5	150 P
U78798_at	9	3	20	20	18 0.45	1.83	0	0 3.0	148 P
X90872_at	12	2	20	20	18 0.60	1.80	0	0 6.0	148 P
U78524_at	7	1	20	20	18 0.35	1.34	1	0 7.0	147 P
X04500_at	9	2	20	20	17 0.45	1.39	0	0 4.5	147 P
X12791_at	12	1	20	20	18 0.60	2.05	0	0 12.0	146 P
X80199_at	12	1	20	20	18 0.60	2.67	0	0 12.0	146 P
X83425_at	9	2	20	20	18 0.45	1.76	0	0 4.5	146 P
X13967_at	9	2	20	20	18 0.45	1.96	0	0 4.5	145 P
X83422_at	9	2	20	20	17 0.45	2.55	0	0 4.5	145 P
X74008_at	9	3	20	20	18 0.45	2.32	1	0 3.0	145 P
X99920_at	12	0	20	20	18 0.60	2.86	1	0 Inf	145 P
Z50022_at	12	1	20	20	18 0.60	1.68	0	0 12.0	145 P
X74795_at	11	3	20	20	17 0.55	2.46	0	0 3.7	143 P
X68733_ma1_at	8	0	20	20	18 0.40	1.30	0	0 Inf	142 P
X76534_at	15	0	20	20	17 0.75	4.86	1	0 Inf	142 P
X82456_at	15	0	20	20	18 0.75	3.78	1	0 Inf	142 P
Z47727_at	12	0	20	20	18 0.60	2.81	0	0 Inf	142 P
U82010_ma1_at	12	0	20	20	18 0.80	2.54	1	0 Inf	141 P
U70451_at	7	1	20	20	18 0.35	1.19	0	0 7.0	139 P
X17620_at	8	2	20	20	18 0.40	1.31	0	0 4.0	139 P
X76770_at	13	1	20	20	18 0.65	3.07	0	0 13.0	139 P
AFFX-HUMRGE/M10098_5_at	10	2	20	20	18 0.50	2.39	0	0 5.0	139 P
U88063_at	14	0	20	20	18 0.70	3.15	0	0 Inf	137 P

Side 5

Connective tissue C									
U77948_at	14	0	20	20	18 0.70	3.86	0	0 Inf	137 P
D50405_at	11	1	20	20	18 0.55	1.94	0	0 11.0	137 P
HG651-IT4201_at	7	0	20	20	18 0.35	1.44	0	0 Inf	136 P
U89338_cds3_at	10	0	20	20	18 0.50	1.83	0	0 Inf	134 P
X76342_at	13	2	20	20	18 0.65	2.84	0	0 6.5	132 P
X54232_at	10	1	20	20	17 0.50	1.70	0	0 10.0	131 P
X70476_at	12	0	20	20	17 0.60	2.84	1	0 Inf	131 P
U68488_at	9	1	20	20	18 0.45	1.34	0	0 9.0	130 P
X01060_at	14	2	20	20	18 0.70	2.96	0	0 7.0	130 P
X14675_at	8	0	20	20	18 0.45	1.41	0	0 Inf	130 P
Y10032_at	14	4	20	20	18 0.70	2.96	3	1 3.5	130 P
D16105_at	8	1	20	20	18 0.40	1.31	0	0 8.0	130 P
U86070_at	11	3	20	20	18 0.55	1.48	0	0 3.7	128 P
Z24725_at	15	0	20	20	18 0.75	4.60	2	0 Inf	128 P
X52882_at	11	0	20	20	18 0.55	2.22	0	0 Inf	127 P
L00058_at	10	0	20	20	18 0.50	2.95	1	0 Inf	127 P
U86915_at	10	1	20	20	18 0.50	1.94	0	0 10.0	126 P
X64364_at	7	0	20	20	17 0.35	1.30	0	0 Inf	126 P
X86779_at	7	0	20	20	17 0.35	1.19	0	0 Inf	125 P
Z84721_cds2_at	12	4	20	20	18 0.60	1.58	0	0 3.0	125 P
X03656_ma1_at	10	2	20	20	17 0.50	1.82	1	0 5.0	124 P
X82895_at	9	1	20	20	18 0.45	1.91	0	0 9.0	124 P
Y09616_at	12	2	20	20	17 0.60	2.08	0	0 6.0	121 P
U67784_at	10	1	20	20	18 0.50	1.97	0	0 10.0	120 P
U80040_at	11	2	20	20	18 0.55	1.66	0	0 5.5	120 P
X72755_at	16	2	20	20	17 0.80	3.68	0	0 8.0	120 P
X60592_at	10	2	20	20	18 0.50	1.12	0	0 5.0	118 P
AFFX-HUMISGF3A/M97935_3_at	12	1	20	20	18 0.60	3.01	2	0 12.0	118 P
U78793_at	10	2	20	20	17 0.50	2.45	0	0 5.0	118 P
X12451_at	12	0	20	20	18 0.60	3.43	2	0 Inf	118 P
X75342_at	11	2	20	20	17 0.55	1.51	0	0 5.5	117 P
X01630_at	10	1	20	20	18 0.50	2.24	1	0 10.0	114 P
X82153_at	13	0	20	20	18 0.65	2.42	0	0 Inf	114 P
L11066_at	7	1	20	20	18 0.35	0.93	0	0 7.0	114 P
U90426_at	12	0	20	20	18 0.60	3.55	1	0 Inf	113 P
U91932_at	11	1	20	20	17 0.55	2.45	0	0 11.0	113 P
X92098_at	10	0	20	20	18 0.50	2.12	0	0 Inf	113 P
Y08134_at	8	1	20	20	18 0.40	1.74	0	0 8.0	112 P
U79260_at	7	0	20	20	18 0.35	1.62	0	0 Inf	112 P
U89336_cds1_at	10	1	20	20	18 0.50	2.01	0	0 10.0	112 P
X05409_at	7	1	20	20	18 0.35	1.29	0	0 7.0	112 P
X95735_at	10	1	20	20	18 0.50	1.85	1	0 10.0	112 P
Y11681_at	8	1	20	20	18 0.40	1.40	0	0 8.0	112 P
U97105_at	12	0	20	20	18 0.60	2.89	0	0 Inf	111 P
X03934_at	10	0	20	20	17 0.50	1.55	0	0 Inf	111 P
X61123_at	14	0	20	20	17 0.70	4.15	2	0 Inf	111 P
X73113_at	9	2	20	20	18 0.45	1.12	0	0 4.5	111 P
X86163_at	11	1	20	20	18 0.55	2.44	0	0 11.0	111 P
U79267_at	14	0	20	20	17 0.70	2.31	0	0 Inf	110 P
X15414_at	10	0	20	20	17 0.50	1.76	0	0 Inf	110 P
U82671_cds2_at	8	0	20	20	18 0.40	1.72	0	0 Inf	109 P
X99728_at	9	2	20	20	18 0.45	1.44	0	0 4.5	109 P

Side 6

Connective tissue C

L10413_at	12	1	20	20	18.60	1.98	0	0	0.12.0	109 P
U78262_at	10	3	20	20	18.50	1.67	0	0	0.3.3	106 P
U78556_at	11	1	20	20	18.55	2.08	0	0	0.11.0	104 P
Z50194_at	12	2	20	20	18.60	2.75	1	0	0.8.0	103 P
X16416_at	7	1	20	20	18.35	1.51	0	0	0.7.0	102 P
X70340_at	7	0	20	20	18.35	1.68	0	0	0 Inf	101 P
Y00815_at	12	0	20	20	18.60	2.85	1	0	0 Inf	101 P
X62744_at	7	2	20	20	18.35	1.34	0	0	0.3.5	100 P
X65873_at	12	3	20	20	18.60	2.43	1	0	0.4.0	100 P
X02530_at	9	1	20	20	18.45	2.34	0	0	0.9.0	99 P
X71874_cds1_at	8	1	20	20	18.40	1.24	0	0	0.8.0	99 P
U90913_at	9	0	20	20	18.45	1.97	0	0	0 Inf	98 P
Z35093_at	8	1	20	20	18.45	1.74	0	0	0.8.0	98 P
Z36531_at	13	2	20	20	18.65	2.63	0	0	0.6.5	98 P
Z48042_at	10	1	20	20	18.50	1.45	0	0	0.10.0	98 P
X62200_at	10	2	20	20	18.50	2.28	0	0	0.5.0	97 P
X06323_at	16	0	20	20	18.80	3.63	0	0	0 Inf	96 P
X52151_at	9	1	20	20	18.45	1.37	0	0	0.9.0	96 P
U83463_at	12	1	20	20	17.60	3.70	2	0	0.12.0	95 P
X93499_at	10	1	20	20	17.50	2.14	0	0	0.11.0	95 P
HG2743-HT2845_at	10	1	20	20	17.50	2.62	2	0	0.10.0	95 P
X74295_at	9	1	20	20	18.45	0.94	0	0	0.9.0	94 P
X80695_at	9	2	20	20	18.45	1.32	0	0	0.4.5	94 P
X92744_at	9	0	20	20	17.45	1.72	0	0	0 Inf	94 P
Z47087_at	14	1	20	20	17.70	3.25	0	0	0.14.0	94 P
U6782_at	14	0	20	20	18.00	3.19	0	0	0 Inf	94 P
X77794_at	14	1	20	20	17.70	3.63	1	0	0.14.0	93 P
U89278_at	8	2	20	20	18.40	0.85	0	0	0.4.0	91 P
X78732_at	13	0	20	20	18.65	3.90	0	0	0 Inf	91 P
X80810_at	10	0	20	20	18.50	2.51	0	0	0 Inf	91 P
U81802_at	7	1	20	20	18.35	1.52	0	0	0.7.0	90 P
X66401_cds1_at	12	1	20	20	18.60	2.65	0	0	0.12.0	90 P
X97302_at	8	0	20	20	17.40	1.60	0	0	0 Inf	90 P
X54942_at	11	1	20	20	18.55	2.13	1	0	0.11.0	89 P
X62466_at	8	2	20	20	17.00	2.09	0	0	0.4.0	89 P
X76104_at	7	2	20	20	18.35	1.34	0	0	0.3.5	89 P
X81003_at	11	0	20	20	18.55	2.07	0	0	0 Inf	89 P
X98283_at	13	0	20	20	17.65	2.37	0	0	0 Inf	89 P
U79287_at	8	0	20	20	18.40	1.56	0	0	0 Inf	88 P
U88602_at	8	1	20	20	18.45	1.57	0	0	0.8.0	88 P
X57766_at	9	2	20	20	18.60	1.69	1	0	0.4.5	88 P
Y08999_at	12	2	20	20	18.00	2.04	2	0	0.6.0	88 P
U72209_at	9	2	20	20	17.45	1.32	1	0	0.4.5	87 P
X65372_at	11	1	20	20	18.55	2.53	1	0	0.11.0	87 P
Y08915_at	9	0	20	20	18.45	1.86	0	0	0 Inf	87 P
U90919_at	13	0	20	20	18.65	3.25	0	0	0 Inf	86 P
X64830_at	11	1	20	20	18.55	1.77	0	0	0.11.0	84 P
Z69720_at	9	2	20	20	18.45	1.51	0	0	0.4.5	83 P
U82130_at	12	0	20	20	18.60	2.44	0	0	0 Inf	82 P
U90909_at	12	0	20	20	18.60	3.01	0	0	0 Inf	82 P
X78925_at	10	1	20	20	18.50	2.34	1	0	0.10.0	82 P
U90716_at	7	1	20	20	18.35	1.53	0	0	0.7.0	81 P

Connective tissue C											
X98261_at	9	2	20	20	18.045	1.18	0	0.45	81 P		
AFFX-M27830_5_at	7	0	20	20	18.035	1.44	0	0 Inf	80 P		
U90547_at	10	1	20	20	17.050	2.10	1	1 10.0	80 P		
X66364_at	8	1	20	20	18.040	0.91	0	0.80	80 P		
Z22548_at	8	1	20	20	17.040	1.97	0	0.80	80 P		
Z50853_at	11	2	20	20	18.055	1.81	0	0.55	80 P		
X78520_at	9	0	20	20	18.045	1.63	0	0 Inf	79 P		
U96113_at	11	1	20	20	18.055	3.13	1	0 11.0	78 P		
X68560_at	10	0	20	20	18.050	2.62	0	0 Inf	78 P		
Z37166_at	10	0	20	20	17.050	1.47	0	0 Inf	78 P		
U81006_at	10	0	20	20	18.050	3.41	1	0 Inf	76 P		
U81607_at	9	1	20	20	18.045	2.66	2	0.90	76 P		
U60911_at	10	0	20	20	18.050	3.00	0	0 Inf	76 P		
X56807_at	8	2	20	20	18.040	1.60	0	0.40	76 P		
X68141_at	11	1	20	20	18.055	2.22	0	0 11.0	76 P		
X93921_at	9	3	20	20	18.045	1.61	0	0.30	76 P		
X87176_at	8	2	20	20	18.045	1.61	0	0.45	75 P		
Z23064_at	10	2	20	20	18.050	2.21	0	0.50	75 P		
X61100_ma1_at	11	2	20	20	18.055	2.89	1	1.55	74 P		
X63879_at	13	1	20	20	18.065	3.39	2	0 13.0	74 P		
Y12711_at	12	1	20	20	18.060	2.00	2	1 12.0	73 P		
Z72498_at	10	2	20	20	17.050	2.51	1	0.50	73 P		
X63973_at	8	2	20	20	18.040	1.78	0	0.40	72 P		
X64373_at	12	0	20	20	18.060	3.15	1	0 Inf	72 P		
Y08614_at	7	2	20	20	18.035	1.33	0	0.35	72 P		
Z29064_at	11	1	20	20	18.055	2.56	0	0 11.0	72 P		
U80017_ma3_at	11	0	20	20	18.055	2.55	1	0 Inf	71 P		
X72177_ma1_at	11	3	20	20	18.055	1.45	0	0.37	71 P		
X80230_at	10	1	20	20	18.050	2.04	1	0 10.0	71 P		
X63753_at	10	1	20	20	18.050	2.63	1	0 10.0	70 P		
X64330_at	9	2	20	20	18.045	1.59	0	0.45	70 P		
X81198_at	7	1	20	20	18.035	2.33	1	0.70	70 P		
X63378_at	10	2	20	20	17.050	1.88	0	0.50	70 P		
X98001_at	8	1	20	20	18.040	1.30	0	0.80	70 P		
U65928_at	13	1	20	20	18.065	1.82	0	0 13.0	69 P		
U70426_at	8	2	20	20	18.040	1.24	0	0.40	69 P		
X79353_at	7	1	20	20	18.035	1.61	1	0.70	69 P		
U76992_at	9	2	20	20	18.045	1.85	1	0.45	68 P		
U87408_at	7	1	20	20	18.035	1.05	0	0.70	68 P		
X07767_at	7	2	20	20	17.035	1.41	0	0.35	68 P		
X63563_at	10	2	20	20	18.035	2.04	1	0.70	68 P		
Y07867_at	7	1	20	20	18.050	2.61	0	0.50	67 P		
X77548_at	8	2	20	20	18.040	1.43	1	0.70	67 P		
Y11306_ma1_at	8	2	20	20	18.040	1.81	1	1.40	67 P		
Z22865_at	8	2	20	20	18.040	1.48	0	0.40	67 P		
AFFX-B10B-3_at	11	1	20	20	18.055	1.24	0	0 11.0	66 P		
X57522_at	11	3	20	20	18.055	2.04	0	0.37	65 P		
X91768_at	12	3	20	20	18.060	2.03	0	0.40	65 P		
U91327_at	8	2	20	20	17.040	2.45	1	0.40	64 P		
U77665_at	8	0	20	20	18.040	1.25	1	0 Inf	63 P		
X03635_at	11	2	20	20	18.055	1.87	0	0.55	63 P		
X58798_at	7	2	20	20	18.035	1.34	0	0.35	63 P		

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Connective tissue C									
X72841_at	13	1	20	20	18.085	3.41	1	0.13.0	63 P
X99325_at	8	1	20	20	18.040	1.08	0	0.8.0	63 P
U76369_at	8	1	20	20	18.040	1.26	1	0.8.0	62 P
X66397_at	11	0	20	20	17.055	2.33	0	0 Inf	62 P
X59405_at	9	2	20	20	18.045	2.15	0	0.4.5	61 P
Z68204_at	7	0	20	20	18.035	1.69	0	0 Inf	61 P
U79297_at	11	1	20	20	18.055	3.42	2	0.11.0	60 P
X16354_at	11	2	20	20	18.055	2.01	0	0.5.5	60 P
X78627_at	11	3	20	20	18.055	2.48	0	0.3.7	60 P
X55544_at	8	1	20	20	18.040	2.20	0	0.8.0	59 P
Y09443_at	7	0	20	20	18.035	1.56	0	0 Inf	59 P
U72508_at	7	1	20	20	18.035	1.24	0	0.7.0	58 P
U73682_at	8	2	20	20	18.040	1.16	0	0.4.0	58 P
U90549_at	8	2	20	20	18.040	1.45	0	0.4.0	58 P
X53586_ma1_at	11	0	20	20	18.055	4.12	2	0 Inf	57 P
-17227_at	10	2	20	20	18.050	1.95	1	0.5.0	57 P
Z67212_at	9	2	20	20	18.045	2.58	1	0.4.5	55 P
K13482_at	7	1	20	20	18.035	1.10	0	0.7.0	54 P
X63469_at	7	0	20	20	18.035	1.85	0	0 Inf	54 P
U69141_at	7	1	20	20	18.035	1.20	0	0.7.0	53 P
U71207_at	9	3	20	20	18.045	1.54	0	0.3.0	53 P
U85992_at	9	2	20	20	18.045	1.82	0	0.4.5	52 P
U79274_at	8	1	20	20	18.040	1.17	0	0.8.0	51 P
U79291_at	13	0	20	20	17.065	4.11	3	0 Inf	50 P
X63337_at	9	2	20	20	18.045	1.31	0	0.4.5	50 P
X64229_at	10	3	20	20	18.050	1.38	1	0.3.3	50 P
Z29331_at	11	2	20	20	18.055	3.99	3	0.5.5	50 P
Z35491_at	8	0	20	20	17.040	2.75	1	0 Inf	50 P
X16396_at	9	0	20	20	18.045	2.61	1	0 Inf	48 P
X60673_ma1_at	9	2	20	20	18.045	1.80	0	0.4.5	48 P
U66669_at	9	2	20	20	18.045	1.83	0	0.4.5	48 P
U72342_at	10	3	20	20	18.050	1.41	0	0.3.3	48 P
U83908_at	9	2	20	20	18.045	2.41	1	0.4.5	48 P
X82396_at	8	2	20	20	18.040	2.11	1	0.4.0	48 P
D86550_at	9	0	20	20	18.045	2.24	0	0 Inf	48 P
X76648_at	9	1	20	20	18.045	2.11	0	0.9.0	47 P
Z88129_cd9s1_at	7	1	20	20	18.035	1.03	0	0.7.0	47 P
D10040_at	8	2	20	20	18.040	1.31	0	0.4.0	47 P
U84573_at	9	1	20	20	18.045	3.00	2	0.9.0	46 P
X54941_at	7	1	20	20	18.035	1.30	0	0.7.0	46 P
X78057_at	8	2	20	20	18.040	1.11	0	0.4.0	46 P
X98248_ma1_at	8	2	20	20	18.040	1.99	1	0.4.0	46 P
Z24724_at	10	0	20	20	18.050	2.59	1	0 Inf	46 P
U68111_at	8	0	20	20	18.045	1.75	0	0 Inf	45 P
U94332_at	7	1	20	20	18.035	1.71	1	0.7.0	45 P
X98172_at	8	0	20	20	18.045	1.23	0	0 Inf	45 P
X62048_at	8	0	20	20	18.040	1.87	0	0 Inf	44 P
X87241_at	10	2	20	20	18.050	2.53	0	0.5.0	44 P
X94232_at	8	0	20	20	17.040	1.63	0	0 Inf	44 P
Z95624_at	7	0	20	20	18.035	1.20	0	0 Inf	44 P
X04011_at	10	2	20	20	18.050	1.47	0	0.5.0	43 P
X98260_at	8	2	20	20	18.040	1.02	0	0.4.0	43 P

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Connective tissue C									
X59841_at	8	0	20	20	18 0.40	1.55	0	0 Inf	42 P
X85644_at	7	1	20	20	17 0.35	0.97	0	0.70	42 P
X74262_at	9	2	20	20	18 0.45	2.21	0	0.45	42 P
X86586_at	8	1	20	20	18 0.45	1.20	0	0.80	42 P
X67319_at	7	1	20	20	18 0.35	0.93	1	0.70	41 P
X07024_at	8	1	20	20	18 0.40	1.31	0	0.80	41 P
X52520_at	9	1	20	20	18 0.45	2.59	0	0.90	41 P
X0912_at	8	1	20	20	18 0.40	1.12	0	0.80	40 P
X06946_at	8	2	20	20	18 0.40	1.65	1	0.40	40 P
X61118_mai_at	10	0	20	20	18 0.50	2.33	0	0 Inf	40 P
X81788_at	11	3	20	20	18 0.55	2.32	1	0.37	40 P
X53793_at	10	2	20	20	18 0.50	2.40	0	0.50	39 P
X54326_at	8	2	20	20	17 0.40	1.00	0	0.40	39 P
X08666_at	8	2	20	20	18 0.40	1.58	1	0.40	37 P
X73608_at	7	1	20	20	18 0.35	1.62	0	0.70	37 P
X84002_at	8	2	20	20	18 0.40	1.58	0	0.40	37 P
X69127_at	8	0	20	20	18 0.40	1.33	0	0 Inf	35 P
X17025_at	8	2	20	20	17 0.40	1.78	1	0.40	35 P
X57206_at	8	2	20	20	18 0.40	1.15	0	0.40	35 P
X76061_at	8	2	20	20	18 0.40	2.02	1	0.40	35 P
Z34897_at	8	1	20	20	18 0.40	1.45	0	0.80	35 P
Z37976_at	8	0	20	20	17 0.40	0.95	0	0 Inf	35 P
X57303_at	8	1	20	20	17 0.40	1.94	0	0.80	34 P
X83368_at	10	2	20	20	18 0.50	2.16	2	0.50	34 P
X10313_at	8	2	20	20	18 0.40	1.25	0	0.40	34 P
X63417_at	7	1	20	20	18 0.35	1.43	0	0.70	33 P
X94910_at	8	1	20	20	18 0.40	1.26	0	0.80	32 P
X77718_at	9	2	20	20	18 0.45	1.27	0	0.45	31 P
X0916_at	10	2	20	20	18 0.50	3.47	3	0.50	31 P
X06562_at	9	2	20	20	18 0.45	2.44	1	0.45	31 P
X73960_at	9	2	20	20	17 0.45	1.15	0	0.45	30 P
X07820_at	8	1	20	20	17 0.35	1.86	1	0.80	30 P
X57025_at	7	0	20	20	18 0.40	1.51	0	0 Inf	30 P
D16481_at	8	1	20	20	18 0.40	1.23	0	0.80	29 P
X75679_at	8	1	20	20	18 0.40	1.51	0	0.80	29 P
X64195_at	7	2	20	20	18 0.35	2.65	2	0.35	29 P
Z46973_at	8	2	20	20	18 0.40	1.73	1	0.40	28 P
X79258_at	8	1	20	20	18 0.40	2.27	0	0.80	27 P
X58723_at	9	2	20	20	18 0.45	2.60	1	0.45	27 P
X92110_at	8	2	20	20	18 0.40	2.38	2	0.40	27 P
X99584_at	7	1	20	20	18 0.35	1.22	0	0.70	27 P
Z22535_at	8	2	20	20	17 0.40	1.20	0	0.40	27 P
U92015_at	8	2	20	20	18 0.40	1.13	0	0.40	26 P
X73882_at	8	2	20	20	18 0.40	1.58	0	0.40	26 P
U79245_at	8	2	20	20	17 0.40	2.65	2	0.40	25 P
X95592_at	10	2	20	20	17 0.50	1.79	0	0.50	25 P
U86561_at	7	2	20	20	18 0.35	1.32	0	0.35	23 P
U97018_at	9	3	20	20	18 0.45	1.38	1	0.30	22 P

Gene Name	Connective tissue D										Abn Cell
	Positiv	Nega	Pos	Pos	Pos	Pos	Pos	Pos	Pos	Pos	
	17	0	19	19	17	0.89	5.63	2	0	Inf	15733 P
M26311_s_at	19	0	20	20	19	0.95	4.86	0	0	Inf	13355 P
X52426_s_at	20	0	20	20	18	1.00	6.88	2	0	Inf	10368 P
M69757_s_at	20	0	20	20	18	1.00	5.41	1	0	Inf	6544 P
L05187_at	62	0	69	69	66	0.90	4.64	2	0	Inf	5698 P
L04483_s_at	18	0	17	17	15	0.94	6.22	3	0	Inf	5632 P
L42601_f_at	19	0	20	20	18	0.95	5.80	2	0	Inf	5155 P
L42563_f_at	20	0	20	20	18	1.00	6.01	3	0	Inf	4939 P
J04617_s_at	17	0	18	18	16	0.94	5.76	1	0	Inf	4935 P
V01516_f_at	19	0	20	20	18	0.85	8.01	2	0	Inf	4779 P
M63438_s_at	15	0	17	17	15	0.88	5.15	0	0	Inf	4579 P
L05188_f_at	19	0	20	20	16	0.95	6.42	2	0	Inf	4465 P
M19888_at	19	0	20	20	18	0.95	6.24	3	0	Inf	4441 P
X53065_f_at	20	0	20	20	18	1.00	5.72	1	0	Inf	4285 P
AFFX-HSAC07/X00351_M_at	20	0	20	20	18	1.00	5.33	0	0	Inf	4239 P
X03689_s_at	18	0	18	18	17	1.00	7.09	1	0	Inf	4233 P
X00351_f_at	19	0	20	20	18	0.95	7.19	2	0	Inf	4186 P
AFFX-HUNGAPDH/M33197_3_at	19	0	20	20	18	0.95	5.82	1	0	Inf	4106 P
X09482_f_at	2	0	3	3	3	0.67	2.08	0	0	Inf	3885 P
M20030_f_at	20	0	20	20	18	1.00	6.64	4	0	Inf	3809 P
M10277_s_at	19	0	20	20	18	0.95	5.59	3	0	Inf	3788 P
J00105_s_at	20	0	20	20	18	1.00	6.04	5	0	Inf	3684 P
X76223_s_at	18	1	20	20	18	0.90	4.92	1	1	18.0	3490 P
M87769_s_at	18	1	20	20	18	0.90	4.97	1	0	18.0	3447 P
HC2815-HT4023_s_at	19	0	20	20	18	0.95	5.41	1	0	Inf	3415 P
01677_f_at	19	0	20	20	18	0.95	5.08	1	0	Inf	3234 P
14199_s_at	20	0	20	20	18	1.00	6.09	1	0	Inf	3222 P
FFX-CrxX-3_at	19	0	20	20	18	0.95	6.81	2	0	Inf	3203 P
157348_s_at	15	0	19	19	17	0.78	4.47	1	0	Inf	3031 P
AFFX-HSAC07/X00351_3_at	17	0	20	20	18	0.85	5.00	0	0	Inf	2862 P
D49824_s_at	7	0	7	7	7	1.00	5.51	0	0	Inf	2821 P
U43901_ma1_e_at	18	0	20	20	18	0.90	5.08	0	0	Inf	2812 P
V00384_s_at	11	0	12	12	10	0.92	6.41	1	0	Inf	2805 P
AFFX-HSAC07/X00351_5_at	18	0	20	20	18	0.90	5.13	0	0	Inf	2776 P
D13413_ma1_s_at	17	0	18	18	16	0.94	5.38	0	0	Inf	2651 P
U08155_s_at	12	1	14	14	12	0.86	5.03	0	1	12.0	2575 P
AFFX-CrxX-5_at	19	0	20	20	18	0.95	7.16	2	0	Inf	2535 P
AFFX-HUNGAPDH/M33197_M_at	16	1	20	20	18	0.80	4.41	0	0	16.0	2457 P
S82287_at	19	0	20	20	18	0.95	4.22	0	0	Inf	2360 P
Z49148_s_at	20	0	20	20	18	1.00	5.62	1	0	Inf	2303 P
HG2815-HT2931_at	5	0	6	6	6	0.83	4.17	0	0	Inf	2265 P
M31520_ma1_s_at	15	0	16	16	14	0.94	6.19	2	0	Inf	2242 P
M34516_at	5	0	5	5	5	1.00	4.11	0	0	Inf	2235 P
M36072_at	16	0	20	20	18	0.80	4.10	0	0	Inf	2150 P
AFFX-HUNGAPDH/M33197_5_at	18	0	20	20	18	0.90	5.78	3	0	Inf	2104 P
M65409_s_at	18	0	20	20	18	0.90	5.84	3	0	Inf	1992 P
L42611_f_at	14	0	20	20	18	0.70	3.86	0	0	Inf	1946 P
X57351_s_at	12	0	12	12	10	1.00	5.81	0	0	Inf	1945 P
HG2815-HT2931_s_at	13	0	14	14	12	0.93	6.37	0	0	Inf	1926 P
X53296_s_at	19	0	20	20	18	0.85	5.49	3	0	Inf	1652 P
M55898_s_at	18	0	20	20	18	0.80	6.05	2	0	Inf	1610 P
X04470_s_at	18	0	19	19	17	0.95	5.06	1	0	Inf	1525 P

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		Connective tissue D											
		17	0	20	20	18.85	3.86	0	0	Inf	1522 P		
M24485_s_at		16	0	20	20	18.80	3.68	1	0	Inf	1473 P		
S71043_mai1_s_at		16	1	20	20	18.80	5.18	3	0	16.0	1446 P		
X51345_at		18	0	20	20	18.90	5.56	2	0	Inf	1416 P		
HG4059-HT4339_s_at		16	1	20	20	18.80	6.79	5	1	16.0	1399 P		
Y07909_at		18	0	20	20	18.90	5.26	1	0	Inf	1311 P		
J04152_mai1_s_at		16	1	19	19	17.84	5.15	0	0	16.0	1263 P		
Z48501_s_at		16	1	20	20	18.85	5.37	0	0	17.0	1239 P		
S68896_at		17	1	20	20	18.70	3.13	0	0	7.0	1215 P		
AFFX-BioDn-3_at		14	2	20	20	18.75	4.09	1	0	7.5	1204 P		
X56681_s_at		15	2	20	20	18.75	5.25	0	0	Inf	1195 P		
U19557_s_at		20	0	20	20	18.100	5.89	1	1	16.0	1186 P		
U19564_g_at		16	1	18	18	16.89	5.92	1	0	Inf	1175 P		
S54005_s_at		19	0	20	20	18.95	6.45	6	0	Inf	1173 P		
U68105_s_at		15	0	20	20	18.75	5.40	2	0	Inf	1172 P		
HG417-HT417_s_at		18	0	20	20	18.85	5.80	1	0	Inf	1126 P		
HG3431-HT3616_s_at		30	0	40	40	38.75	3.63	0	0	Inf	1085 P		
M84880_f_at		17	1	20	20	18.85	2.94	0	0	17.0	1072 P		
S72493_s_at		16	0	20	20	18.80	3.73	1	0	Inf	1069 P		
U20734_s_at		11	0	11	11	9.100	5.23	1	0	Inf	1058 P		
M34516_r_at		17	0	20	20	18.85	4.74	0	0	Inf	1050 P		
X68654_at		19	0	20	20	18.95	5.73	1	0	Inf	1028 P		
M92843_s_at		15	0	20	20	18.75	3.95	0	0	Inf	952 P		
M13560_s_at		15	0	20	20	18.75	2.92	0	0	Inf	941 P		
U57341_f_at		1	0	2	2	2.050	4.28	0	0	15.0	917 P		
L33830_s_at		15	1	20	20	18.75	5.11	3	0	Inf	911 P		
M26708_s_at		18	0	20	20	18.90	4.90	0	0	Inf	903 P		
X04347_s_at		12	0	20	20	18.60	2.78	0	0	Inf	889 P		
HG1880-HT2023_at		30	0	40	40	38.75	3.12	2	0	17.0	842 P		
HG658-HT658_f_at		17	1	20	20	18.85	5.16	0	0	Inf	838 P		
M11313_s_at		17	0	20	20	18.85	3.60	0	0	12.0	822 P		
M83687_mai1_s_at		12	1	18	16	14.075	5.56	0	0	14.0	818 P		
M19311_s_at		14	1	20	20	18.070	3.92	0	0	Inf	802 P		
M14328_s_at		5	0	8	8	8.63	2.90	0	0	Inf	782 P		
X57351_at		13	0	19	19	17.68	2.94	0	0	6.5	779 P		
U06643_s_at		13	2	20	20	18.65	3.48	0	0	15.0	759 P		
N21142_cd32_s_at		15	1	20	20	18.75	3.28	0	0	Inf	737 P		
Z68228_s_at		15	0	19	19	17.79	3.82	0	0	Inf	715 P		
HG2787-HT2905_s_at		17	0	20	20	18.85	4.75	0	0	9.0	662 P		
D32129_f_at		9	1	12	12	10.75	2.45	0	0	3.0	660 P		
X57809_s_at		3	1	8	8	8.38	2.72	2	0	Inf	655 P		
V00594_at		16	0	20	20	18.80	5.27	0	0	Inf	644 P		
HG1515-HT1515_f_at		16	0	19	19	17.84	4.66	3	0	17.0	640 P		
HG3342-HT3519_s_at		17	1	20	20	18.85	4.50	4	0	14.0	629 P		
S75256_s_at		14	1	20	20	18.70	4.81	0	0	Inf	619 P		
M18045_f_at		13	0	20	20	18.65	3.12	0	0	3.3	602 P		
M14463_mai1_s_at		10	3	20	20	17.90	2.07	0	0	Inf	594 P		
Z30643_at		15	0	20	20	18.75	3.82	4	1	6.5	589 P		
AFFX-HSAC07X00351_3_at		13	2	20	20	18.65	3.73	0	0	Inf			
X95240_s_at		16	0	20	20	18.60	3.73	0	0	Inf			
M33600_f_at		13	2	20	20	18.65	4.15	3	0	6.5			
X14008_mai1_f_at		14	1	20	20	18.70	4.11	2	0	14.0			
M21302_at		20	0	20	20	18.100	4.55	0	0	Inf			
X12671_mai1_at		11	1	19	19	17.058	3.30	1	0	11.0			
L12711_s_at													

Side 2

Connective tissue D																			
M12125_at	12	2	20	20	18 0.60	2.30	0	0.0	586 P										
M58026_at	10	1	20	20	18 0.50	2.18	0	0 10.0	573 P										
J03801_f_at	13	1	20	20	18 0.65	5.62	3	0 13.0	557 P										
D86974_at	15	2	20	20	18 0.75	2.56	0	0 7.5	519 P										
J03077_s_at	11	1	20	20	18 0.55	3.21	0	0 11.0	510 P										
M54915_s_at	13	0	20	20	18 0.65	3.37	0	0 Inf	500 P										
HG3236-HT3413_f_at	12	1	20	20	18 0.60	3.01	0	0 12.0	490 P										
D17408_s_at	14	0	20	20	18 0.70	3.72	0	0 Inf	483 P										
M26730_s_at	17	1	20	20	18 0.85	5.65	2	0 17.0	465 P										
X05130_s_at	12	2	19	19	17 0.63	2.54	0	1 6.0	464 P										
U14394_at	11	3	20	20	18 0.55	2.95	0	0 3.7	456 P										
X17093_at	12	1	20	20	18 0.60	2.73	1	0 12.0	435 P										
L33075_at	17	0	20	20	18 0.85	4.20	1	0 Inf	432 P										
HG3597-HT3800_f_at	15	1	20	20	17 0.75	4.30	2	0 15.0	422 P										
U43916_s_at	15	0	20	20	18 0.75	3.48	0	0 Inf	408 P										
L40397_at	12	1	20	20	18 0.60	2.35	0	0 12.0	407 P										
HG1428-HT1428_s_at	15	0	20	20	18 0.75	4.25	1	0 Inf	401 P										
X02761_s_at	14	0	20	20	18 0.70	3.69	0	0 Inf	397 P										
X12876_s_at	15	1	20	20	18 0.75	4.25	0	0 15.0	385 P										
X99133_at	9	2	20	20	18 0.45	1.79	0	0 4.5	384 P										
L11672_at	6	0	12	12	10 0.50	2.17	0	0 Inf	370 P										
HG2917-HT3051_f_at	12	0	20	20	18 0.60	2.29	0	0 Inf	370 P										
HG3576-HT3779_f_at	11	2	20	20	18 0.55	2.86	0	0 5.5	365 P										
U00947_s_at	19	0	20	20	18 0.95	5.49	3	0 Inf	361 P										
HG2916-HT3059_f_at	10	0	20	20	17 0.50	2.22	0	0 Inf	351 P										
Z48835_s_at	14	3	20	20	18 0.70	3.25	1	1 4.7	349 P										
HG2994-HT4850_s_at	8	2	20	20	18 0.40	1.29	0	0 4.0	348 P										
D43682_s_at	9	3	20	20	18 0.45	2.40	0	0 3.0	345 P										
Z69043_s_at	16	1	20	20	18 0.80	3.44	0	0 7.0	344 P										
AFFX-BloDn-5_at	14	2	20	20	18 0.70	2.39	0	0 10.0	342 P										
X95325_s_at	11	3	20	20	18 0.55	1.91	0	0 3.7	340 P										
HG1322-HT5143_s_at	14	1	20	20	18 0.70	4.19	0	0 14.0	339 P										
AFFX-BloC-5_at	16	1	20	20	18 0.80	3.17	0	0 16.0	337 P										
J02683_s_at	11	0	20	20	18 0.55	2.60	0	0 Inf	337 P										
M62403_s_at	12	1	20	20	18 0.60	2.19	0	0 Inf	327 P										
U48705_maf_s_at	12	1	20	20	18 0.60	3.02	1	0 12.0	327 P										
M33493_s_at	12	1	20	20	18 0.60	3.10	1	0 12.0	313 P										
U92314_s_at	14	4	20	20	18 0.70	2.77	0	0 3.5	311 P										
X15729_s_at	16	2	20	20	18 0.80	4.10	1	0 8.0	305 P										
U05861_at	14	0	20	20	18 0.70	3.11	0	0 Inf	297 P										
X13461_s_at	9	2	20	20	18 0.45	1.93	0	0 4.5	296 P										
U70439_s_at	12	1	20	20	18 0.60	2.88	0	0 12.0	288 P										
M19267_s_at	9	1	19	19	17 0.47	2.77	2	0 9.0	284 P										
L09209_s_at	13	1	20	20	18 0.65	2.85	0	0 13.0	279 P										
V00589_s_at	13	2	20	20	18 0.65	2.04	0	0 6.5	278 P										
M18750_s_at	13	0	20	20	18 0.85	3.30	0	0 Inf	277 P										
M64046_at	7	0	20	20	18 0.35	1.76	0	0 Inf	270 P										
M65292_s_at	14	1	20	20	18 0.70	3.97	0	0 14.0	251 P										
M12953_s_at	9	0	15	15	17 0.47	3.02	0	0 Inf	248 P										
M13690_s_at	10	0	20	20	17 0.50	2.40	1	0 Inf	248 P										
U72649_at	14	1	20	20	18 0.70	2.43	0	0 14.0	244 P										
M28213_s_at	17	0	20	20	18 0.85	4.88	1	0 Inf	241 P										
HG3076-HT3238_s_at	14	0	20	20	17 0.70	3.31	1	0 Inf	239 P										
M30448_s_at	12	2	20	20	17 0.60	2.84	0	0 6.0	239 P										

Side 3

Connective tissue D																			
M34986_s_at	17	0	20	20	18 0.85	4.33	1	0 Inf	232 P										
D17793_at	14	2	20	20	18 0.70	2.78	0	0 7.0	232 P										
X52022_at	13	1	20	20	17 0.65	2.97	0	0 13.0	231 P										
X06700_s_at	16	0	20	20	18 0.80	4.50	2	0 Inf	229 P										
Y00787_s_at	12	0	20	20	18 0.60	2.65	0	0 Inf	224 P										
D16799_s_at	14	2	20	20	18 0.70	3.85	2	0 7.0	223 P										
X57152_rna1_s_at	14	2	20	20	18 0.70	2.80	0	0 7.0	223 P										
D87017_cd63_at	8	0	20	20	18 0.40	1.43	0	0 Inf	222 P										
U05681_s_at	12	2	20	20	18 0.60	1.94	0	0 6.0	221 P										
M31551_s_at	13	1	20	20	18 0.65	3.30	1	1 13.0	219 P										
X01703_at	14	2	20	20	18 0.70	2.83	1	0 7.0	218 P										
J02621_s_at	11	0	20	20	18 0.55	2.51	1	0 Inf	217 P										
M21538_at	13	0	20	20	18 0.65	2.60	1	0 Inf	215 P										
L13740_at	7	0	20	20	18 0.35	1.21	0	0 Inf	212 P										
X52979_rna1_s_at	14	1	20	20	18 0.70	2.51	0	0 14.0	209 P										
M27438_s_at	13	0	20	20	18 0.65	3.39	0	0 Inf	206 P										
J03805_s_at	16	0	18	18	16 0.89	5.53	3	0 Inf	206 P										
X17587_s_at	10	2	20	20	17 0.50	2.32	0	0 5.0	206 P										
M32304_s_at	9	2	20	20	18 0.45	1.56	0	0 4.5	202 P										
M16342_at	13	1	20	20	17 0.65	2.88	0	0 13.0	201 P										
M16652_at	3	0	4	4	4 0.75	2.05	0	0 Inf	201 P										
X03066_f_at	18	3	40	40	38 0.45	1.61	0	0 6.0	194 P										
M23223_s_at	11	2	20	20	18 0.55	1.80	0	0 5.5	192 P										
K02405_f_at	10	2	20	20	18 0.50	1.27	0	0 5.0	182 P										
HG4535-HT4940_s_at	8	1	20	20	18 0.40	1.14	0	0 8.0	181 P										
M57466_s_at	9	2	20	20	18 0.45	2.18	0	0 4.5	188 P										
M97835_s_at	13	2	20	20	18 0.65	2.71	0	0 6.5	186 P										
X04528_at	14	1	20	20	18 0.70	2.32	0	0 14.0	185 P										
M29874_s_at	13	2	20	20	18 0.65	2.72	0	0 6.5	185 P										
U04636_rna1_at	11	1	20	20	18 0.55	1.99	0	1 11.0	184 P										
Z15115_at	14	2	20	20	18 0.70	2.33	0	0 7.0	184 P										
X72727_at	15	1	20	20	18 0.75	3.16	0	0 15.0	183 P										
Y00264_at	13	1	20	20	17 0.85	3.58	0	0 13.0	183 P										
AFFX-BioC-3_at	11	0	20	20	18 0.55	1.90	0	0 Inf	175 P										
HG3044-HT3742_s_at	11	0	20	20	18 0.55	2.78	0	0 Inf	175 P										
U61734_s_at	10	1	19	19	17 0.53	2.84	1	0 10.0	175 P										
L49380_at	8	2	20	20	18 0.40	1.18	0	0 4.0	171 P										
D10667_s_at	14	1	17	17	15 0.82	3.23	0	0 14.0	170 P										
D78577_s_at	11	1	20	20	18 0.55	2.47	2	0 11.0	169 P										
D83174_g_at	9	0	20	20	17 0.45	1.86	0	0 Inf	168 P										
M37457_at	3	0	4	4	4 0.75	2.10	0	0 Inf	167 P										
D78132_s_at	14	0	20	20	18 0.70	5.12	2	0 Inf	166 P										
X71345_f_at	9	2	20	20	18 0.45	1.93	1	0 4.5	165 P										
U08021_at	10	0	20	20	17 0.50	2.15	0	0 Inf	164 P										
U01691_s_at	9	0	20	20	18 0.45	3.00	3	0 Inf	163 P										
M3216_s_at	15	1	20	20	18 0.75	3.89	0	0 15.0	163 P										
HG688-HT688_f_at	10	1	20	20	18 0.50	1.61	0	0 10.0	160 P										
M30703_g_at	10	1	20	20	18 0.35	2.67	1	1 10.0	160 P										
U79528_s_at	7	0	20	20	18 0.50	1.46	0	0 Inf	159 P										
M93651_at	10	0	20	20	18 0.50	2.68	1	0 Inf	159 P										
HG4541-H14946_s_at	10	0	18	18	16 0.56	2.35	0	0 Inf	159 P										
X73358_s_at	9	1	19	19	17 0.47	1.75	1	0 9.0	159 P										
Z35402_rna1_s_at	10	1	20	20	18 0.50	2.27	0	0 10.0	159 P										
U12767_at	13	0	20	20	17 0.65	2.37	0	0 Inf	154 P										

Side 4

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[illegible]

Side 5

Connective tissue D											
U35341_rna1_at	7	1	20	20	18 0.35	1.08	0	0.7.0	98 P		
U22431_s_at	12	1	20	20	17 0.60	2.37	0	0.12.0	88 P		
M60874_s_at	7	0	20	20	17 0.35	1.28	0	0. Inf	98 P		
AFFX-BioB-5_at	8	2	20	20	18 0.40	1.15	0	0.4.0	95 P		
D42040_s_at	8	2	20	20	18 0.40	1.51	0	0.4.0	94 P		
U67122_s_at	11	1	20	20	18 0.55	2.43	0	0.11.0	94 P		
U28014_at	13	0	20	20	18 0.65	3.23	1	0. Inf	94 P		
D78206_s_at	8	0	20	20	17 0.40	1.32	0	0. Inf	93 P		
S78771_s_at	10	3	20	20	18 0.50	1.91	0	0.3.3	92 P		
M58525_s_at	7	1	20	20	18 0.35	1.20	0	0.7.0	92 P		
M60483_rna1_s_at	9	1	18	18	16 0.50	2.65	1	0.9.0	92 P		
HG2868-HT3012_s_at	9	2	20	20	18 0.45	2.18	1	0.4.5	91 P		
U41518_at	10	0	20	20	18 0.50	1.67	0	0. Inf	90 P		
Z74615_at	8	1	20	20	17 0.40	1.76	1	0.8.0	90 P		
Z35085_s_at	14	1	18	18	17 0.74	4.26	1	0.14.0	80 P		
L76517_at	7	0	20	20	17 0.35	1.61	0	0. Inf	89 P		
M16276_at	9	1	20	20	18 0.45	1.76	0	0.9.0	89 P		
D45917_s_at	10	2	20	20	18 0.50	2.13	2	1.5.0	88 P		
U19495_s_at	15	1	20	20	17 0.75	4.92	4	0.15.0	88 P		
X07438_s_at	14	2	19	19	17 0.74	3.49	1	0.7.0	88 P		
U41740_at	12	2	20	20	18 0.60	2.58	1	0.6.0	86 P		
X03363_s_at	9	1	20	20	18 0.45	1.54	0	0.8.0	86 P		
M28882_s_at	8	1	17	17	15 0.47	2.28	1	0.8.0	85 P		
HG4322-HT4582_at	11	2	20	20	18 0.55	2.59	1	0.5.5	85 P		
L38490_s_at	7	1	20	20	18 0.35	1.30	0	0.7.0	84 P		
X62083_s_at	7	1	20	20	18 0.35	1.31	1	0.7.0	84 P		
U43944_at	12	1	20	20	18 0.60	2.44	0	0.12.0	84 P		
HG33484-HT3878_s_at	9	0	20	20	18 0.45	2.10	0	0. Inf	83 P		
X62534_s_at	10	0	20	20	18 0.50	2.63	0	0. Inf	83 P		
Y00097_s_at	8	2	20	20	18 0.40	1.73	0	0.4.0	82 P		
S72024_s_at	8	1	20	20	18 0.40	1.57	0	0.8.0	82 P		
U72509_s_at	10	1	18	19	16 0.53	2.19	0	0.10.0	82 P		
X65488_at	12	0	20	20	18 0.60	2.37	1	0. Inf	81 P		
L32831_s_at	11	2	20	20	18 0.55	1.13	0	0.5.5	81 P		
U45448_s_at	10	3	20	20	18 0.50	1.88	0	0.3.3	81 P		
M20867_s_at	9	1	17	17	14 0.53	1.70	0	0.9.0	78 P		
U30827_s_at	13	1	20	20	17 0.65	3.56	2	0.13.0	79 P		
M31832_at	8	2	20	20	18 0.40	1.12	0	0.4.0	79 P		
Z69030_s_at	6	1	18	18	16 0.33	1.85	1	0.6.0	78 P		
HG3638-HT3849_s_at	9	1	20	20	18 0.45	1.88	1	0.8.0	77 P		
U35005_s_at	10	2	20	20	18 0.50	2.08	0	0.5.0	76 P		
HG2981-HT3127_s_at	11	1	19	19	17 0.58	1.75	0	0.11.0	75 P		
D14826_s_at	7	1	20	20	18 0.35	1.19	0	0.7.0	74 P		
M63838_s_at	8	0	20	20	18 0.45	2.69	1	0. Inf	73 P		
Y00451_s_at	8	0	20	20	18 0.40	1.34	0	0. Inf	73 P		
U19247_rna1_s_at	10	2	20	20	18 0.50	2.37	0	0.5.0	72 P		
J04093_s_at	10	0	20	20	18 0.50	1.92	0	0. Inf	72 P		
X60003_s_at	9	2	20	20	18 0.45	1.58	0	0.4.5	72 P		
M61832_s_at	8	2	20	20	18 0.40	1.11	0	0.4.0	71 P		
U01337_at	7	1	20	20	18 0.35	1.14	0	0.7.0	68 P		
Z28491_s_at	10	0	20	20	18 0.50	2.52	1	0. Inf	66 P		
U33936_s_at	12	2	20	20	18 0.60	1.80	0	0.6.0	66 P		
S68805_at	10	0	20	20	18 0.50	2.36	0	0. Inf	65 P		
D83260_s_at	8	1	19	19	16 0.42	1.83	0	0.8.0	65 P		

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Connective tissue D

U20938_at	11	0	20	20	18 0.55	1.93	0	0 Inf	64 P
HG1400-HT1400_s_at	11	2	20	20	18 0.55	2.42	0	0 5.5	63 P
L14778_s_at	12	0	19	19	17 0.63	4.34	4	0 Inf	61 P
U96131_at	8	1	20	20	18 0.40	1.46	1	0 8.0	60 P
M17183_s_at	8	1	20	20	18 0.40	1.95	1	0 8.0	60 P
L00634_s_at	10	1	19	19	17 0.53	3.14	2	0 10.0	60 P
U56046_s_at	12	1	20	20	18 0.60	3.04	1	0 12.0	58 P
X53002_s_at	8	2	20	20	18 0.40	1.14	0	0 4.0	59 P
X69820_s_at	8	1	20	20	18 0.40	2.17	0	0 8.0	59 P
U33062_s_at	8	0	20	20	17 0.40	3.36	1	0 Inf	59 P
U44103_at	10	2	20	20	17 0.50	2.57	0	0 5.0	59 P
D28473_s_at	10	2	20	20	18 0.50	2.16	0	0 5.0	58 P
U60061_at	9	2	20	20	18 0.45	2.22	2	0 4.5	57 P
M21119_s_at	7	1	20	20	18 0.35	0.54	0	0 7.0	57 P
U33838_at	2	0	4	4	4 0.50	2.70	0	0 Inf	57 P
M24736_s_at	7	1	20	20	18 0.35	1.12	0	0 7.0	57 P
HG4518-HT4821_t_at	1	0	2	2	2 0.50	1.26	0	0 Inf	56 P
HG4557-HT4962_f_at	3	0	5	5	5 0.60	1.88	0	0 Inf	56 P
S77410_at	7	1	20	20	18 0.35	1.04	0	0 7.0	55 P
HG2090-HT2152_s_at	7	2	19	19	17 0.37	1.63	1	1 3.5	55 P
X81625_at	9	1	20	20	18 0.45	2.01	1	0 9.0	54 P
U41766_s_at	8	2	20	20	18 0.40	1.27	1	0 4.0	53 P
U61276_s_at	9	2	20	20	18 0.45	2.01	0	0 4.5	53 P
Y07566_at	9	1	20	20	18 0.45	1.50	0	0 9.0	53 P
U33632_at	12	1	20	20	17 0.60	3.09	1	0 12.0	52 P
M10321_s_at	7	1	20	20	18 0.35	1.12	0	0 7.0	52 P
J03834_s_at	9	2	20	20	18 0.45	1.91	0	0 4.5	51 P
X14253_s_at	8	2	20	20	18 0.40	1.76	0	0 4.0	51 P
L15326_s_at	10	1	20	20	18 0.50	1.91	0	0 10.0	50 P
M75715_s_at	9	1	19	19	17 0.47	2.08	0	0 8.0	50 P
L08010_at	8	2	20	20	17 0.40	1.72	0	0 4.0	50 P
M31516_s_at	7	0	20	20	18 0.35	1.37	0	0 Inf	49 P
M96843_at	8	2	20	20	18 0.40	0.99	0	0 4.0	48 P
X75918_at	11	2	20	20	18 0.55	1.77	0	0 5.5	48 P
D28235_s_at	10	1	20	20	18 0.50	1.49	0	0 10.0	47 P
M18508_xpt3_s_at	8	1	20	20	18 0.40	0.95	0	0 8.0	47 P
S79219_s_at	9	3	20	20	18 0.45	1.79	0	0 3.0	46 P
L35249_s_at	7	1	18	18	16 0.39	1.78	0	0 7.0	45 P
U84388_at	10	0	20	20	18 0.50	3.54	1	0 Inf	45 P
AFFX-HUMTFR/M11507_s_at	9	2	20	20	18 0.45	1.08	0	0 4.5	44 P
HG2743-HT3926_s_at	12	1	20	20	18 0.60	1.82	0	0 12.0	44 P
HG545-HT345_s_at	9	2	20	20	18 0.45	1.08	0	0 4.5	44 P
U69140_s_at	7	1	18	18	16 0.39	2.73	1	0 7.0	44 P
AFFX-HUMRGE/M10098_M1_at	7	1	20	20	18 0.35	1.75	0	0 7.0	42 P
U73936_at	8	2	20	20	18 0.40	1.14	0	0 4.0	42 P
AB000381_s_at	9	2	20	20	18 0.45	2.66	2	0 4.5	42 P
M28610_at	9	2	14	14	12 0.64	4.77	4	0 4.5	42 P
U04265_s_at	8	3	20	20	17 0.35	1.90	1	0 3.0	42 P
HG3075-HT3236_s_at	7	2	20	20	17 0.45	1.57	2	0 3.5	40 P
X54993_s_at	8	2	20	20	18 0.40	1.29	1	0 4.0	40 P
U61397_s_at	7	1	20	20	18 0.35	1.56	0	0 7.0	40 P
X99886_s_at	7	0	19	19	17 0.37	1.26	0	0 Inf	40 P
S82597_ma1_s_at	9	1	20	20	18 0.45	1.21	0	0 9.0	39 P
X06182_s_at	8	1	20	20	18 0.40	1.48	1	0 8.0	38 P

Side 7

Normal urothelium A

Pos/Neg Pair Pos Fr Log Av P M Pos/N Avg Diff Abs Call

Gene Name

hum_ali_at	69	0	69	69	67	1.00	7.39	12	0	Inf	27021 P
.06499_at	20	0	20	20	18	1.00	7.57	3	0	Inf	12530 P
h33214-HT3391_at	19	0	20	20	18	0.95	7.36	4	0	Inf	8561 P
AFFX-CreX-3_at	19	0	20	20	18	0.95	8.08	2	0	Inf	5961 P
HG3384-HT3541_at	20	0	20	20	18	1.00	7.78	7	0	Inf	5937 P
M13934_cds2_at	19	0	20	20	18	0.95	6.91	1	0	Inf	5721 P
HG1800-HT1823_at	19	0	20	20	18	0.95	7.88	4	0	Inf	5403 P
M17888_at	18	0	20	20	18	0.90	5.81	1	0	Inf	5130 P
M11147_at	18	0	20	20	18	0.90	6.85	3	0	Inf	4610 P
D45370_at	19	0	20	20	18	0.95	5.40	2	0	Inf	4549 P
HG2873-HT3017_at	18	0	20	20	18	0.90	7.15	3	0	Inf	4508 P
AFFX-CreX-5_at	20	0	20	20	18	1.00	7.29	4	0	Inf	4443 P
M18000_at	20	0	20	20	18	1.00	8.01	6	0	Inf	4368 P
D23660_at	19	0	20	20	18	0.95	7.99	6	0	Inf	4257 P
L06505_at	17	0	20	20	18	0.85	5.35	2	0	Inf	4184 P
HG3548-HT3751_at	19	0	20	20	18	0.95	6.73	3	0	Inf	4127 P
M17885_at	19	1	20	20	18	0.95	6.97	2	0	19.0	3868 P
AFFX-HUMIGAPDH/M331	19	0	20	20	18	0.95	5.62	1	0	Inf	3862 P
L38941_at	20	0	20	20	18	1.00	8.04	5	0	Inf	3734 P
AFFX-BigDn-3_at	17	0	20	20	18	0.85	4.18	0	0	Inf	3458 P
HG2789-HT2896_at	18	0	20	20	18	0.90	6.08	1	0	Inf	3126 P
M17733_at	18	0	20	20	18	0.90	6.92	3	0	Inf	2882 P
D79205_at	20	0	20	20	18	1.00	8.85	8	0	Inf	2864 P
L19527_at	18	0	20	20	18	0.90	5.82	2	0	Inf	2522 P
D78361_at	18	0	20	20	18	0.90	5.73	0	0	Inf	2513 P
AFFX-HSAC07/X00351_2	18	0	20	20	18	0.90	5.45	1	0	Inf	2382 P
D14530_at	20	0	20	20	18	1.00	7.43	3	0	Inf	2301 P
HG821-HT821_at	18	0	20	20	18	0.90	5.85	2	0	Inf	1918 P
HG813-HT613_at	18	0	20	20	17	0.95	6.85	5	0	Inf	1834 P
HG4319-HT4569_at	19	0	20	20	18	0.95	6.06	1	0	Inf	1746 P
HG384-HT384_at	12	0	20	20	17	0.60	4.27	2	0	Inf	1634 P
L20941_at	15	0	20	20	17	0.75	3.62	1	0	Inf	1530 P
HG4542-HT4847_at	17	0	20	20	18	0.85	5.16	1	0	Inf	1500 P
HG311-HT311_at	18	1	20	20	17	0.90	6.14	3	0	18.0	1484 P
AC002115_cds1_at	16	0	20	20	18	0.80	4.81	0	0	Inf	1456 P
AC002115_cds4_at	16	0	20	20	18	0.80	3.23	0	0	Inf	1382 P
M11353_at	16	1	20	20	17	0.80	6.14	3	0	16.0	1359 P
HG33-HT33_at	18	0	20	20	17	0.90	5.44	1	0	Inf	1327 P
D00017_at	16	0	20	20	18	0.80	4.46	0	0	Inf	1293 P
L11568_at	14	0	20	20	18	0.70	3.86	0	0	Inf	1195 P
D87735_at	17	0	20	20	17	0.85	4.52	1	0	Inf	1192 P
AFFX-HSAC07/X00351_A	18	1	20	20	18	0.90	3.90	0	0	18.0	1181 P
J04164_at	11	2	20	20	18	0.55	2.83	2	0	5.5	1186 P
J03592_at	17	1	20	20	18	0.85	4.77	1	0	17.0	1140 P
HG862-HT682_at	9	2	20	20	18	0.45	2.67	0	0	4.5	955 P
L19686_ma1_at	14	2	20	20	18	0.70	3.02	0	0	7.0	919 P
L26247_at	15	0	20	20	18	0.75	4.10	0	0	Inf	888 P

Side 1

Normal urothelium A

HG2279-HT2375_at	16	0	20	20	18	0.80	2.80	1	0	Inf	872 P
D89667_at	17	1	20	20	18	0.85	5.25	0	0	Inf	842 P
D38583_at	18	1	20	20	18	0.90	4.35	1	0	18.0	841 P
AFFX-HSAC07X00351_5	16	1	20	20	18	0.80	4.03	1	0	16.0	829 P
D00554_at	15	0	20	20	18	0.75	3.92	1	0	Inf	751 P
D30655_at	14	0	20	20	18	0.70	4.02	1	0	Inf	728 P
AFFX-HUMGAPDH/M331	14	2	20	20	18	0.70	2.59	0	0	7.0	725 P
M18283_at	15	2	20	20	18	0.75	3.61	1	0	7.5	725 P
M18961_at	14	3	20	20	18	0.70	2.67	2	0	4.7	705 P
J03827_at	13	0	20	20	18	0.65	3.12	0	0	Inf	694 P
AFFX-BioDn-5_at	11	0	20	20	18	0.55	2.70	0	0	Inf	692 P
D63874_at	12	1	20	20	18	0.60	3.74	3	0	12.0	675 P
J03181_at	17	0	20	20	18	0.85	4.97	0	0	Inf	668 P
J04823_ma1_at	15	1	20	20	18	0.75	3.33	0	0	15.0	638 P
K03460_at	9	0	20	20	18	0.45	2.81	0	0	Inf	632 P
D29012_at	12	3	20	20	18	0.60	2.49	0	0	4.0	628 P
D14710_at	15	0	20	20	18	0.75	3.42	2	0	Inf	613 P
D45248_at	14	1	20	20	18	0.70	3.48	0	0	14.0	603 P
M15661_at	17	1	20	20	18	0.85	3.85	0	0	17.0	600 P
HG1153-HT1153_at	13	1	20	20	18	0.65	3.12	0	0	13.0	583 P
D28124_at	14	0	20	20	18	0.70	2.85	0	0	Inf	580 P
J04988_at	14	0	20	20	18	0.70	3.69	1	0	Inf	578 P
AFFX-BioC-5_at	15	1	20	20	18	0.75	2.89	0	0	15.0	557 P
K02765_at	15	0	20	20	18	0.75	2.97	1	0	Inf	540 P
J02854_at	11	0	20	20	18	0.55	2.21	0	0	Inf	522 P
D13118_at	9	1	20	20	18	0.45	2.11	1	0	9.0	501 P
D23662_at	14	1	20	20	18	0.70	2.87	0	0	14.0	496 P
D29863_at	13	1	20	20	18	0.65	2.14	0	0	13.0	482 P
D00761_at	15	0	20	20	18	0.75	2.92	0	0	Inf	462 P
M12529_at	9	1	20	20	18	0.45	2.16	0	0	9.0	448 P
L12168_at	10	0	20	20	18	0.50	2.72	0	0	Inf	445 P
M11119_at	9	0	20	20	18	0.45	1.94	0	0	Inf	437 P
D31883_at	10	2	20	20	18	0.50	1.48	0	0	5.0	431 P
D31846_at	10	0	20	20	18	0.50	1.89	0	0	Inf	424 P
M20471_at	15	0	20	20	18	0.75	2.97	0	0	Inf	421 P
D38548_at	9	1	20	20	18	0.45	2.00	0	0	9.0	417 P
J04456_at	16	0	20	20	18	0.80	3.92	1	0	Inf	413 P
AFFX-HUMGAPDH/M331	12	3	20	20	18	0.60	2.01	0	0	4.0	406 P
HG987-HT987_at	15	3	20	20	18	0.75	3.80	2	0	5.0	404 P
D29873_at	11	0	20	20	18	0.55	2.25	0	0	Inf	401 P
AFFX-BioC-3_at	13	0	20	20	18	0.65	2.46	0	0	Inf	381 P
D14520_at	10	1	20	20	18	0.50	2.04	0	0	10.0	387 P
D26598_at	10	0	20	20	18	0.50	2.32	0	0	Inf	384 P
D16562_at	15	1	20	20	17	0.75	4.14	1	0	15.0	364 P
L15702_at	12	2	20	20	18	0.60	1.91	0	0	8.0	363 P
L3842_ma1_at	14	1	20	20	18	0.70	3.38	0	0	14.0	358 P
L38486_at	12	2	20	20	18	0.60	2.38	0	0	6.0	354 P
D13748_at	12	1	20	20	18	0.60	2.07	0	0	12.0	353 P
HG2855-HT2895_at	13	1	20	20	18	0.65	2.94	0	0	13.0	347 P
AFFX-HSAC07X00351_5	12	0	20	20	17	0.60	3.21	0	0	Inf	346 P
D85815_at	11	3	20	20	18	0.55	1.88	0	0	3.7	344 P

Normal urothelium A

D25274_at	11	2	20	20	17	0.55	2.35	0	0.55	342 P
L21954_at	13	4	20	20	18	0.65	2.18	0	0.33	341 P
D63475_at	14	1	20	20	18	0.70	3.17	0	0.140	338 P
M19483_at	13	1	20	20	18	0.65	2.28	0	0.130	338 P
D85429_at	11	1	20	20	18	0.55	2.03	0	0.110	333 P
D83878_at	12	3	20	20	18	0.80	1.71	0	0.40	331 P
D50310_at	18	0	20	20	18	0.90	3.57	0	0 Inf	325 P
D25066_at	10	2	20	20	18	0.50	2.74	1	0.50	323 P
D13640_at	7	2	20	20	18	0.35	1.74	0	0.35	313 P
M16279_at	7	2	20	20	18	0.35	1.59	0	0.35	311 P
D11428_at	7	1	20	20	18	0.35	1.23	0	1.70	309 P
HG2566-HT4867_at	10	2	20	20	18	0.50	1.69	0	0.50	307 P
AF015910_at	8	0	20	20	18	0.40	1.59	0	0 Inf	306 P
L19605_at	12	1	20	20	17	0.60	2.18	0	0.120	305 P
D80209_at	14	1	20	20	18	0.70	3.13	0	0.140	299 P
D38047_at	11	0	20	20	18	0.55	2.10	0	0 Inf	298 P
J04173_at	9	2	20	20	18	0.45	2.20	0	0.45	297 P
M13955_at	11	3	20	20	18	0.55	1.67	0	0.37	295 P
D49400_at	8	1	20	20	18	0.45	1.94	0	0.90	293 P
L09604_at	10	2	20	20	18	0.50	2.00	0	0.50	292 P
AB000584_at	10	2	20	20	18	0.50	1.42	0	0.50	286 P
L76200_at	10	3	20	20	18	0.50	2.12	1	0.33	285 P
J04611_at	10	1	20	20	18	0.50	1.79	0	0.100	279 P
M14200_rna1_at	10	1	20	20	17	0.50	1.88	0	0.100	274 P
HG1614-HT1614_at	8	1	20	20	17	0.45	1.30	0	0.80	272 P
J04794_at	9	3	20	20	18	0.45	1.45	0	0.30	271 P
AF006084_at	11	2	20	20	17	0.55	2.31	0	0.55	269 P
D26599_at	13	2	20	20	18	0.65	2.75	0	0.65	269 P
D50863_at	13	2	20	20	18	0.85	2.43	0	1.65	269 P
D16217_at	11	0	20	20	17	0.55	2.34	0	0 Inf	267 P
J02874_at	12	2	20	20	18	0.60	3.23	2	0.60	267 P
D25216_at	10	1	20	20	17	0.50	2.07	1	0.100	265 P
D55696_at	9	2	20	20	17	0.45	2.27	1	0.45	260 P
D82348_at	11	2	20	20	18	0.55	2.22	0	0.55	258 P
D14694_at	13	0	20	20	18	0.65	2.55	0	0 Inf	255 P
J03600_at	11	2	20	20	18	0.55	2.66	0	0.55	255 P
J03459_at	10	1	20	20	18	0.50	1.97	1	0.100	254 P
L25080_at	10	2	20	20	18	0.50	2.35	1	0.50	250 P
L07633_at	12	0	20	20	18	0.60	3.26	0	0 Inf	249 P
D10522_at	13	1	20	20	18	0.65	3.23	1	0.130	248 P
L02426_at	11	0	20	20	18	0.55	2.00	0	0 Inf	242 P
L10264_at	13	1	20	20	18	0.65	2.61	0	0.130	239 P
M14050_at	11	0	20	20	18	0.55	2.20	0	0 Inf	235 P
L13977_at	12	1	20	20	18	0.60	2.18	0	0.120	232 P
J03069_rna1_at	9	2	20	20	18	0.45	1.95	0	0.45	230 P
M13755_at	7	1	20	20	18	0.35	1.08	0	0.70	230 P
HG1862-HT1897_at	10	2	20	20	18	0.50	2.50	0	0.50	228 P
L13852_at	7	0	20	20	18	0.35	1.48	0	0 Inf	225 P
M12886_at	11	2	20	20	17	0.55	1.57	0	0.55	222 P
D88422_at	11	2	20	20	18	0.55	2.38	0	0.55	221 P
L25081_at	7	0	20	20	18	0.35	1.12	0	0 Inf	219 P

Side 3

Normal urothelium A

D26600_at	15	1	20	20	17	0.75	2.67	0	0	15.0	218 P
L11285_at	9	2	20	20	18	0.45	1.62	0	0	4.5	218 P
L40904_at	7	0	20	20	18	0.35	1.76	0	0	Inf	218 P
HG3484-HT3688_at	8	1	20	20	17	0.40	1.31	0	0	8.0	217 P
D21089_at	10	1	20	20	17	0.50	2.25	1	0	10.0	215 P
D86965_at	8	1	20	20	18	0.40	1.45	0	0	8.0	215 P
L24203_at	11	0	20	20	18	0.55	1.98	0	0	Inf	213 P
M14676_at	9	3	20	20	18	0.45	1.96	0	0	3.0	213 P
K03430_at	9	0	20	20	18	0.45	1.79	0	0	Inf	212 P
L40027_at	10	2	20	20	18	0.50	1.97	1	0	5.0	212 P
D00763_at	11	1	20	20	18	0.55	1.92	0	0	11.0	211 P
L19437_at	10	0	20	20	18	0.50	2.35	1	0	Inf	210 P
HG1076-HT1078_at	14	2	20	20	18	0.70	2.55	0	0	7.0	207 P
L32977_at	14	1	20	20	17	0.70	3.51	1	0	14.0	204 P
D87953_at	11	0	20	20	18	0.55	2.89	0	0	Inf	203 P
AB001325_at	8	2	20	20	18	0.40	0.92	0	0	4.0	200 P
D78134_at	10	2	20	20	17	0.50	2.15	0	0	5.0	200 P
D43642_at	12	1	20	20	18	0.60	2.32	0	0	12.0	187 P
D14682_at	10	1	20	20	18	0.50	2.68	1	0	10.0	191 P
D31884_at	11	2	20	20	18	0.55	1.89	0	0	5.5	191 P
D83542_at	10	3	20	20	18	0.50	1.53	0	0	3.3	191 P
HG3514-HT3708_at	10	1	20	20	18	0.50	2.20	0	0	10.0	191 P
D63486_at	8	0	20	20	17	0.40	1.11	0	0	Inf	190 P
D31890_at	13	1	20	20	17	0.65	3.06	1	0	13.0	186 P
D48738_at	11	3	20	20	18	0.55	1.83	0	0	3.7	186 P
D50063_at	9	2	20	20	18	0.45	1.60	1	1	4.5	183 P
D63160_at	7	0	20	20	18	0.35	1.23	0	0	Inf	178 P
D38305_at	10	0	20	20	17	0.50	2.17	1	0	Inf	176 P
D38048_at	11	1	20	20	18	0.55	2.31	0	0	11.0	173 P
D49387_at	9	1	20	20	18	0.45	2.24	1	0	9.0	173 P
D31765_at	8	1	20	20	18	0.40	1.61	0	0	8.0	172 P
M15182_at	8	2	20	20	18	0.40	1.10	0	0	4.0	171 P
HG4287-HT4567_at	14	2	20	20	18	0.70	2.88	1	0	7.0	170 P
L12350_at	11	0	20	20	18	0.55	2.36	0	0	Inf	170 P
D32050_at	8	2	20	20	18	0.40	1.22	0	0	4.0	168 P
L08246_at	10	2	20	20	18	0.50	1.49	0	1	5.0	166 P
L28010_at	11	1	20	20	18	0.55	2.23	0	0	11.0	165 P
M13450_at	13	0	20	20	18	0.65	2.71	1	0	Inf	165 P
D85245_at	10	2	20	20	18	0.50	2.05	1	0	5.0	160 P
L11708_at	9	3	20	20	18	0.45	1.60	0	0	3.0	159 P
D78991_at	7	1	20	20	18	0.35	1.81	0	0	7.0	158 P
AJ001421_at	10	0	20	20	18	0.50	1.17	0	0	Inf	157 P
D14043_at	11	1	20	20	17	0.55	2.52	0	0	11.0	157 P
D13370_at	10	1	20	20	17	0.50	1.50	0	0	10.0	153 P
K03195_at	10	2	20	20	18	0.50	2.95	3	0	5.0	153 P
L76465_at	11	3	20	20	18	0.55	2.43	2	1	3.7	150 P
D84239_at	10	2	20	20	18	0.50	1.69	0	0	5.0	149 P
D89016_at	8	1	20	20	17	0.40	1.63	0	0	8.0	145 P
M11717_maf1_at	12	3	20	20	18	0.60	2.87	3	1	4.0	146 P
M11726_at	8	1	20	20	18	0.40	1.57	0	0	8.0	145 P
L13197_at	7	0	20	20	18	0.35	1.59	0	0	Inf	144 P

Normal urothelium A

L20773_at	10	3	20	20	18	0.50	1.40	0	0.33	144 P
HG2614-HT12710_at	7	1	20	20	18	0.35	1.29	0	0.70	143 P
L36531_at	9	1	20	20	18	0.45	1.85	0	0.90	142 P
D14686_at	9	2	20	20	18	0.45	1.25	0	0.45	141 P
D55554_at	9	1	20	20	17	0.45	1.51	0	0.90	141 P
HG1102-HT1102_at	7	1	20	20	18	0.35	1.71	0	0.70	140 P
L11669_at	11	2	20	20	17	0.55	1.37	0	0.55	138 P
L38698_at	7	1	20	20	18	0.35	1.20	0	0.70	138 P
L41559_at	8	2	20	20	18	0.40	1.47	0	0.40	138 P
D50911_at	9	2	20	20	18	0.45	1.29	0	0.45	136 P
D38076_at	7	1	20	20	18	0.35	1.43	0	0.70	134 P
D88978_at	13	2	20	20	18	0.65	2.94	2	1.65	133 P
L34587_at	9	1	20	20	18	0.45	1.38	0	0.90	133 P
AF006041_at	11	3	20	20	18	0.55	1.49	0	0.37	132 P
D90276_at	8	1	20	20	18	0.40	1.48	0	0.80	132 P
HG960-HT960_at	10	1	20	20	18	0.50	1.38	0	0.10.0	132 P
L38064_rna1_at	9	2	20	20	18	0.45	1.38	0	0.45	132 P
AC002045_xpt1_at	8	0	20	20	18	0.40	1.50	0	0.1nf	128 P
D50912_at	8	1	20	20	18	0.40	1.42	0	0.80	127 P
D87438_at	8	2	20	20	17	0.40	1.58	0	0.40	127 P
D28915_at	11	0	20	20	18	0.55	2.33	1	0.1nf	125 P
HG1602-HT1602_at	7	1	20	20	18	0.35	0.98	0	0.70	124 P
D21260_at	8	0	20	20	17	0.40	1.58	0	0.1nf	123 P
D83478_at	9	0	20	20	17	0.45	2.17	1	0.1nf	123 P
D80005_at	8	2	20	20	18	0.40	1.84	0	0.40	123 P
D84110_at	14	1	20	20	17	0.70	2.96	2	0.14.0	123 P
.06132_at	9	3	20	20	18	0.45	2.09	2	0.30	122 P
387258_at	9	2	20	20	18	0.45	1.61	0	0.45	121 P
.01396_at	12	2	20	20	18	0.60	1.50	0	0.60	121 P
.07033_at	10	3	20	20	18	0.50	1.98	1	0.33	120 P
298543_at	13	1	20	20	18	0.65	2.42	0	0.13.0	120 P
D50683_at	9	3	20	20	17	0.45	1.94	2	0.30	119 P
D85758_at	7	1	20	20	18	0.35	1.34	0	0.70	118 P
L19779_at	12	2	20	20	18	0.60	3.22	1	0.60	118 P
L27709_at	9	1	20	20	18	0.45	2.17	2	0.90	118 P
L40393_at	7	2	20	20	18	0.35	1.81	3	1.35	117 P
D83032_at	7	2	20	20	18	0.35	1.53	0	0.35	116 P
D30755_at	14	2	20	20	18	0.70	3.79	3	0.70	116 P
D49488_at	7	2	20	20	18	0.35	1.58	1	0.35	116 P
D83782_at	8	0	20	20	18	0.40	1.57	0	0.1nf	115 P
D56495_at	8	2	20	20	18	0.40	0.91	0	0.40	115 P
M13207_at	8	1	20	20	17	0.35	0.94	0	0.70	114 P
D87673_at	7	1	20	20	17	0.35	0.94	0	0.70	114 P
M11437_cds2_at	8	0	20	20	18	0.40	2.10	1	0.1nf	114 P
D21852_at	12	2	20	20	18	0.60	2.95	2	0.80	113 P
L19183_at	8	2	20	20	18	0.40	1.49	0	0.40	113 P
L77888_at	12	4	20	20	18	0.80	2.61	1	0.30	113 P
M18079_at	10	2	20	20	18	0.50	1.91	1	0.50	113 P
D43950_at	7	1	20	20	18	0.35	1.79	0	0.70	111 P
D14658_at	8	1	20	20	18	0.40	1.69	0	0.80	110 P
M18737_rna1_at	8	2	20	20	18	0.40	1.29	1	0.40	110 P

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D78611_at	10	1	20	20	18.050	1.91	1	0	10.0	109 P
L49168_at	10	0	20	20	17.050	1.50	0	0	Inf	108 P
D00760_at	10	1	20	20	18.050	1.53	0	0	10.0	107 P
L08666_at	8	2	20	20	17.040	1.26	0	0	4.0	107 P
AB000115_at	7	1	20	20	18.035	0.97	0	0	7.0	106 P
D79986_at	9	1	20	20	18.045	1.89	1	0	9.0	106 P
D86957_at	12	2	20	20	17.060	2.67	1	1	6.0	106 P
D14663_at	9	0	20	20	18.045	2.11	0	0	Inf	105 P
D42043_at	11	3	20	20	18.055	2.49	0	0	3.7	104 P
M12759_at	9	1	20	20	18.045	1.95	1	0	9.0	104 P
HG3510-HT3704_at	9	0	20	20	18.045	1.50	0	0	Inf	103 P
D90086_at	10	1	20	20	18.050	2.04	1	0	10.0	102 P
D79994_at	8	1	20	20	18.040	1.46	0	0	8.0	101 P
HG4058-HT4328_at	10	3	20	20	18.050	1.62	1	0	3.3	100 P
L21936_at	8	0	20	20	18.040	2.02	1	0	Inf	100 P
M11716_at	8	0	20	20	18.040	1.43	0	0	Inf	100 P
D84454_at	7	1	20	20	18.035	1.27	0	0	7.0	99 P
D21851_at	9	2	20	20	18.045	1.69	1	0	4.5	99 P
HG2274-HT2370_at	8	1	20	20	17.040	1.34	0	0	8.0	98 P
HG4073-HT4343_at	7	1	20	20	18.035	1.22	0	0	7.0	98 P
HG4243-HT4513_at	11	2	20	20	18.055	1.92	1	0	5.5	97 P
HG908-HT908_at	8	1	20	20	18.045	2.08	0	0	9.0	97 P
HG1879-HT1918_at	8	0	20	20	18.045	2.15	1	0	Inf	96 P
L41658_mn1_at	7	1	20	20	17.035	1.22	0	0	7.0	96 P
D50640_at	13	2	20	20	18.065	2.89	2	0	6.5	95 P
HG1869-HT1904_at	9	1	20	20	18.045	1.41	0	0	9.0	95 P
HG2167-HT2237_at	10	2	20	20	18.050	1.82	0	0	5.0	95 P
L13391_at	11	0	20	20	18.055	2.08	0	0	Inf	95 P
L16942_at	8	1	20	20	18.040	0.91	0	0	8.0	95 P
D44466_at	10	1	20	20	18.050	1.47	0	0	10.0	94 P
D49488_at	11	3	20	20	18.055	2.45	1	0	3.7	92 P
D85181_at	11	3	20	20	18.055	2.17	1	0	3.7	92 P
D14878_at	10	2	20	20	18.050	1.95	0	0	5.0	91 P
D86962_at	12	4	20	20	18.060	1.83	0	1	3.0	91 P
D21853_at	7	1	20	20	18.035	1.41	1	0	7.0	90 P
D38549_at	10	3	20	20	17.050	2.39	2	0	3.3	89 P
D84294_at	10	2	20	20	18.050	2.10	2	1	5.0	89 P
D87435_at	8	2	20	20	18.040	1.46	0	0	4.0	88 P
D25278_at	11	2	20	20	17.055	2.02	1	0	5.5	88 P
D79996_at	10	3	20	20	18.050	1.52	1	0	3.3	88 P
L12535_at	8	1	20	20	18.045	3.21	3	0	9.0	88 P
D63480_at	8	1	20	20	18.040	1.90	0	0	6.0	87 P
D79995_at	7	0	20	20	18.035	1.31	0	0	Inf	87 P
L19314_at	7	1	20	20	17.035	1.39	1	0	7.0	87 P
L42378_at	9	3	20	20	18.045	1.74	0	0	3.0	86 P
D30756_at	10	3	20	20	18.050	1.78	2	0	3.3	84 P
D50857_at	8	2	20	20	18.040	1.48	0	0	4.0	84 P
HG1112-HT1112_at	8	0	20	20	17.040	1.25	0	0	Inf	82 P
D83004_at	8	2	20	20	18.040	0.98	0	0	4.0	80 P

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Normal urothelium A

D876B4_at	10	2	20	20	18.0.50	2.64	3	0.5.0	80 P
HG2096-HT1214_at	8	1	20	20	18.0.40	1.45	0	0.8.0	78 P
L29008_at	9	3	20	20	18.0.45	1.64	1	0.3.0	78 P
D28641_at	9	1	20	20	18.0.45	2.71	3	0.9.0	77 P
L18972_at	7	1	20	20	18.0.35	1.12	0	0.7.0	77 P
J04056_at	10	3	20	20	17.0.50	1.73	0	0.3.3	76 P
L40636_at	7	2	20	20	18.0.35	1.43	0	1.3.5	76 P
L24470_at	7	1	20	20	18.0.35	0.96	0	0.7.0	75 P
L40357_at	9	2	20	20	18.0.45	1.40	0	1.4.5	75 P
L27560_at	9	2	20	20	18.0.45	1.59	1	0.4.5	74 P
D13639_at	9	2	20	20	18.0.45	1.59	0	0.4.5	70 P
L43631_at	8	2	20	20	18.0.40	1.65	1	0.4.0	70 P
D28476_at	8	1	20	20	18.0.40	1.63	0	0.8.0	69 P
D42123_at	7	1	20	20	18.0.35	1.11	0	0.7.0	69 P
D88613_at	9	2	20	20	17.0.45	1.98	2	0.4.5	68 P
D17400_at	9	1	20	20	18.0.45	1.53	0	0.9.0	67 P
AFU12270_at	9	1	20	20	18.0.45	1.39	0	0.9.0	65 P
D50827_at	9	2	20	20	18.0.45	1.48	0	0.4.5	85 P
D38521_at	8	2	20	20	17.0.40	1.30	1	0.4.0	64 P
D38553_at	7	2	20	20	18.0.35	1.61	0	0.3.5	64 P
D80006_at	8	1	20	20	18.0.40	2.01	1	0.8.0	64 P
L42542_at	8	1	20	20	17.0.40	1.09	0	0.8.0	83 P
D14695_at	11	2	20	20	18.0.55	1.49	0	0.5.5	82 P
L78703_at	8	2	20	20	18.0.40	1.61	2	0.4.0	62 P
HG4336-HT4606_at	9	2	20	20	18.0.45	1.91	0	0.4.5	61 P
D50917_at	11	3	20	20	18.0.55	2.24	2	1.3.7	58 P
D86885_at	12	3	20	20	18.0.60	1.04	0	1.4.0	58 P
HG4390-HT4660_at	8	1	20	20	18.0.40	1.15	0	0.8.0	58 P
L33881_at	12	4	20	20	18.0.60	1.80	1	0.3.0	58 P
D80004_at	7	1	20	20	17.0.35	1.02	0	0.7.0	57 P
D43767_at	8	2	20	20	17.0.40	0.90	0	0.4.0	55 P
D50525_at	9	2	20	20	17.0.45	2.21	3	0.4.5	55 P
L76380_at	11	3	20	20	18.0.55	1.80	0	0.3.7	55 P
D42087_at	9	3	20	20	18.0.45	2.32	2	1.3.0	54 P
HG2460-HT2556_at	9	3	20	20	18.0.45	1.85	2	0.3.0	50 P
L07515_at	8	2	20	20	18.0.40	1.10	0	0.4.0	50 P
L20581_at	8	2	20	20	18.0.40	1.30	0	2.4.0	50 P
L77563_at	7	2	20	20	18.0.35	1.69	2	0.3.5	50 P
D63412_at	8	1	20	20	18.0.40	1.08	0	0.8.0	48 P
J04162_at	7	2	20	20	18.0.35	1.57	0	0.3.5	48 P
D15050_at	8	1	20	20	17.0.40	0.97	0	0.8.0	45 P
L10123_at	10	2	20	20	18.0.50	2.00	2	0.5.0	45 P
AFX-HUMISGF3AM979	9	3	20	20	18.0.45	1.96	0	0.3.0	44 P
L32163_at	9	3	20	20	18.0.40	1.79	1	0.4.0	42 P
D14664_at	9	3	20	20	18.0.45	1.51	1	1.3.0	41 P
D86425_at	9	3	20	20	18.0.45	2.58	2	0.3.0	37 P
L11885_at	8	2	20	20	18.0.45	1.08	0	0.4.5	34 P
D63875_at	9	2	20	20	18.0.45	1.25	0	0.4.5	29 P
L40388_at	9	1	20	20	18.0.45	1.79	0	0.8.0	23 P
D87443_at	7	2	20	20	18.0.35	1.71	1	0.3.5	22 P

Normal urothelium B

Gene Name	Positive	Negative	Paired	Paired	Log Avg	PM Ex	MMI	Pos/Neg	Avg Diff	Abs Call
hum_allu_at	69	0	69	69	7.55	14	0	Inf	34085 P	
U14973_at	18	0	20	20	18.90	1	0	Inf	6948 P	
AFFX-CreX-3_at	19	1	20	20	18.95	0	0	18.0	5673 P	
U14969_at	20	0	20	20	18.100	1	0	Inf	5259 P	
U14972_at	19	0	20	20	18.085	0	0	Inf	5247 P	
M24194_at	18	0	20	20	18.095	0	0	Inf	4955 P	
M81757_at	18	0	20	20	18.090	1	0	Inf	4759 P	
U14968_at	16	0	20	20	18.080	2	0	Inf	4708 P	
U12465_at	20	0	20	20	18.100	0	0	Inf	4503 P	
M31951_at	15	3	20	20	18.075	7	0	5.0	4128 P	
AFFX-CreX-5_at	20	0	20	20	18.100	1	0	Inf	3983 P	
M60854_at	18	0	20	20	18.090	4	0	Inf	3548 P	
S79522_at	17	0	20	20	18.085	2	0	Inf	3543 P	
M84711_at	17	0	20	20	18.085	0	0	Inf	3365 P	
M84716_at	14	3	20	20	18.070	1	0	4.7	3345 P	
AFFX-HUNGAPDH/M33197_3	19	0	20	20	17.095	1	0	Inf	3257 P	
M77232_ma1_at	18	1	20	20	18.080	1	0	16.0	3217 P	
AFFX-HSAC07/X00351_3_at	16	0	20	20	18.080	4	0	Inf	3110 P	
U49869_ma1_at	19	0	20	20	17.095	2	0	Inf	3081 P	
U58682_at	17	1	20	20	18.085	2	0	17.0	3033 P	
U14971_at	18	0	20	20	18.090	0	0	Inf	2924 P	
U09953_at	18	0	20	20	18.080	3	0	Inf	2871 P	
U14970_at	18	0	20	20	18.090	2	0	Inf	2723 P	
U12404_at	18	0	20	20	18.080	1	0	Inf	2655 P	
M31520_at	17	0	20	20	18.085	1	0	Inf	2526 P	
M32405_at	11	3	20	20	18.055	1	0	3.7	2461 P	
M33680_at	17	0	20	20	18.085	2	0	Inf	2367 P	
M84526_at	13	0	20	20	18.065	0	0	Inf	2281 P	
AFFX-BioDn-3_at	15	2	20	20	17.075	0	0	7.5	2202 P	
U25789_at	17	1	20	20	18.085	0	0	17.0	2092 P	
S73591_at	15	0	20	20	18.075	1	0	Inf	1714 P	
U15008_at	13	2	20	20	18.065	0	0	6.5	1556 P	
M26880_at	15	0	20	20	18.075	2	0	Inf	1454 P	
U31875_at	18	0	20	20	18.080	0	0	Inf	1358 P	
AFFX-HSAC07/X00351_M_at	15	1	20	20	18.075	0	0	15.0	1261 P	
M63138_at	8	1	20	20	18.040	0	0	8.0	1215 P	
M63379_at	15	0	20	20	18.075	1	0	Inf	1169 P	
M57710_at	17	0	20	20	17.085	0	0	Inf	1035 P	
U50523_at	13	3	20	20	18.065	1	1	4.3	946 P	
M95787_at	12	0	20	20	18.060	0	0	Inf	944 P	
AFFX-HSAC07/X00351_5_at	13	1	20	20	18.065	0	0	13.0	943 P	
M27891_at	11	2	20	20	18.055	0	0	5.5	943 P	
U21831_at	14	0	20	20	17.070	3	0	Inf	866 P	
U44839_at	11	3	20	20	18.055	0	0	3.7	805 P	
M23613_at	11	2	20	20	18.055	0	0	5.5	779 P	
M34182_at	12	2	20	20	18.060	0	0	6.0	772 P	
U46692_ma1_at	13	2	20	20	18.065	0	0	6.5	748 P	
U37690_at	12	0	20	20	18.060	0	0	Inf	688 P	
M80563_at	11	0	20	20	18.055	0	0	Inf	678 P	
U41835_at	8	1	20	20	18.040	0	0	8.0	658 P	

Side 1

Normal urothelium B

U46751_at	10	2	20	20	18.0.50	2.76	1	0.5.0	644 P
U03057_at	8	2	20	20	18.0.40	1.23	0	0.4.0	643 P
S65738_at	14	1	20	20	18.0.70	3.33	0	0.14.0	621 P
S77356_at	13	3	20	20	18.0.65	2.78	0	0.4.3	615 P
AFFX-HUMGAPDH/M33187_A	12	3	20	20	17.0.60	2.00	0	0.4.0	614 P
U62739_at	10	2	20	20	18.0.50	1.85	0	0.5.0	612 P
S75463_at	9	2	20	20	18.0.45	1.83	1	0.4.5	598 P
U62982_at	11	2	20	20	18.0.55	2.04	0	0.5.5	595 P
M35878_at	12	3	20	20	18.0.60	1.70	0	1.4.0	577 P
U46570_at	8	1	20	20	18.0.40	1.28	0	0.8.0	550 P
AFFX-HUMGAPDH/M33187_5	12	0	20	20	18.0.60	2.95	0	0. Inf	538 P
U11851_at	10	2	20	20	18.0.50	1.58	0	0.5.0	536 P
M57587_at	10	1	20	20	18.0.50	1.70	0	0.10.0	525 P
U01212_at	10	2	20	20	18.0.50	1.25	0	0.5.0	517 P
U03398_at	10	3	20	20	18.0.50	2.46	2	0.3.3	500 P
U45975_at	7	2	20	20	18.0.35	1.31	0	0.3.5	485 P
U46408_at	10	3	20	20	17.0.50	1.65	0	0.3.3	484 P
M76378_at	8	2	20	20	18.0.40	1.16	0	0.4.0	478 P
M55593_at	10	1	20	20	18.0.50	2.09	1	0.10.0	471 P
U09117_at	7	2	20	20	18.0.35	1.38	0	0.3.5	464 P
U46025_at	11	2	20	20	18.0.55	1.76	1	0.5.5	463 P
U51478_at	13	1	20	20	18.0.65	3.39	0	0.13.0	459 P
M28877_at	10	0	20	20	18.0.50	1.79	1	0. Inf	457 P
M32053_at	9	1	20	20	18.0.45	1.90	0	0.9.0	452 P
AFFX-BioC-5_at	8	1	20	20	18.0.40	1.19	0	0.8.0	434 P
U08813_at	12	1	20	20	18.0.60	2.90	0	0.12.0	434 P
M87815_at	9	2	20	20	18.0.45	1.38	0	0.4.5	431 P
M88279_at	11	0	20	20	18.0.55	2.28	0	0. Inf	428 P
S73149_at	8	1	20	20	18.0.40	1.14	0	0.8.0	424 P
M84349_at	11	2	20	20	18.0.55	2.40	0	0.5.5	415 P
U29656_at	7	0	20	20	18.0.35	1.70	0	0. Inf	412 P
U37689_at	10	0	20	20	18.0.50	1.42	0	0. Inf	408 P
M22382_at	9	0	20	20	18.0.45	1.45	0	0. Inf	396 P
S68616_at	8	2	20	20	18.0.40	1.37	0	0.4.0	381 P
M85400_at	11	1	20	20	18.0.55	2.44	1	0.11.0	387 P
U57342_at	9	1	20	20	18.0.45	1.93	0	0.9.0	387 P
M60858_ma1_at	10	2	20	20	18.0.50	2.42	0	0.5.0	376 P
AFFX-BioOn-5_at	8	0	20	20	18.0.45	1.37	0	0. Inf	373 P
M84332_at	10	1	20	20	18.0.50	1.49	0	0.10.0	370 P
M38590_at	10	0	20	20	18.0.50	2.51	1	0. Inf	367 P
M22538_at	7	0	20	20	18.0.35	1.00	0	0. Inf	365 P
U57450_at	10	0	20	20	18.0.50	1.17	0	0. Inf	365 P
U30825_at	11	3	20	20	18.0.55	1.59	0	0.3.7	355 P
M75126_at	9	1	20	20	18.0.45	1.67	0	0.9.0	347 P
M95627_at	7	0	20	20	18.0.35	1.50	0	0. Inf	344 P
U50138_ma1_at	8	2	20	20	18.0.40	1.16	0	0.4.0	338 P
U14603_at	12	0	20	20	18.0.80	2.58	0	0. Inf	337 P
M75099_at	9	0	20	20	18.0.45	2.03	0	0. Inf	336 P
U33821_at	10	1	20	20	18.0.50	1.67	0	0.10.0	327 P
U21128_at	12	3	20	20	18.0.60	2.20	1	1.4.0	324 P
M28713_at	7	1	20	20	18.0.35	1.35	0	0.7.0	321 P
U37519_at	7	2	20	20	18.0.35	1.88	0	0.3.5	

Side 2

Normal urothelium B									
M73547_at	12	4	20	20	18.060	2.03	1	0.30	318 P
M95803_at	12	2	20	20	18.060	1.31	0	1.80	310 P
U41371_at	12	1	20	20	18.060	2.45	0	0.12.0	310 P
AFFX-HSAC07X00351_3_at	13	0	20	20	17.065	2.19	0	0 Inf	303 P
M94345_at	10	2	20	20	18.050	1.48	0	0.50	302 P
U02493_at	8	0	20	20	18.040	1.74	0	0 Inf	302 P
M58285_at	8	0	20	20	18.040	1.16	0	0 Inf	293 P
U02570_at	7	1	20	20	18.035	1.53	0	0.70	283 P
AFFX-BloC-3_at	7	1	20	20	18.035	1.33	0	0.70	292 P
M62831_at	8	0	20	20	18.040	1.16	0	0 Inf	281 P
U32944_at	13	1	20	20	18.065	3.00	2	0.13.0	290 P
U52522_at	7	2	20	20	18.035	1.74	0	0.35	208 P
M88338_at	7	1	20	20	18.035	0.87	0	0.70	283 P
M77349_at	14	0	20	20	18.070	2.49	0	0 Inf	277 P
U29607_at	13	3	20	20	18.065	2.26	2	1.43	278 P
M31303_maf1_at	9	2	20	20	18.045	1.63	0	0.45	274 P
M66439_at	11	1	20	20	18.055	2.84	2	0.11.0	271 P
M63959_at	10	2	20	20	18.050	1.26	0	0.50	270 P
M24899_at	10	2	20	20	18.050	1.58	0	0.50	269 P
U07857_at	13	2	20	20	17.065	2.51	0	1.65	269 P
U30888_at	10	2	20	20	18.050	1.49	0	0.50	266 P
M81780_cds5_at	8	1	20	20	18.040	1.13	0	0.80	258 P
M23254_at	11	3	20	20	17.055	1.84	0	0.37	256 P
U05658_at	10	2	20	20	18.050	1.74	1	1.50	256 P
U49785_at	12	1	20	20	18.060	2.29	0	0.12.0	256 P
U10323_at	10	1	20	20	17.050	2.08	0	0.10.0	254 P
M64347_at	7	1	20	20	18.035	1.70	2	1.70	253 P
U20285_at	9	2	20	20	18.045	1.32	0	0.45	246 P
U43286_at	11	0	20	20	18.055	2.55	1	0 Inf	246 P
M82809_at	13	1	20	20	18.065	2.26	0	0.13.0	243 P
M96859_at	10	3	20	20	18.050	2.22	1	0.33	243 P
U56637_at	7	2	20	20	17.035	1.37	0	1.35	240 P
U40890_at	7	0	20	20	18.035	1.09	0	0 Inf	238 P
U48092_at	8	2	20	20	18.040	0.83	0	0.40	227 P
M91029_cds2_at	7	2	20	20	18.035	1.32	0	0.35	224 P
U52100_at	7	1	20	20	18.035	1.25	0	0.70	224 P
U40998_at	8	2	20	20	18.040	1.32	0	0.40	221 P
M90299_at	8	2	20	20	18.040	1.20	0	0.40	220 P
S71824_at	7	1	20	20	18.035	1.30	0	0.70	220 P
M31627_at	11	2	20	20	18.055	1.69	0	0.55	219 P
M83751_at	7	2	20	20	17.035	1.46	0	0.35	219 P
U43077_at	8	1	20	20	18.040	1.58	0	0.80	215 P
M20960_at	10	2	20	20	18.050	1.52	2	0.50	215 P
M92449_at	10	2	20	20	18.050	1.94	1	0.50	212 P
M29536_at	11	2	20	20	18.055	1.95	0	0.55	207 P
S81083_cds1_at	7	1	20	20	18.035	1.07	0	0.70	207 P
M81601_at	7	1	20	20	18.035	1.55	0	0.70	205 P
U50535_at	11	3	20	20	18.055	2.10	0	0.37	203 P
M87284_at	9	2	20	20	18.045	1.41	0	0.45	202 P
U24152_at	7	2	20	20	18.035	1.43	0	0.35	198 P
U51678_at	10	3	20	20	18.050	1.77	0	0.33	189 P
M64571_at	9	2	20	20	18.045	1.43	0	0.45	187 P

Side 3

Normal urothelium B

574017_at	10	2	20	20	18 0.50	1.59	0	0.50	195 P
U38846_at	8	1	20	20	18 0.40	1.39	0	0.80	196 P
M32313_at	9	1	20	20	18 0.45	1.62	1	0.90	194 P
U43148_at	8	1	20	20	18 0.40	1.08	0	0.80	191 P
M55543_at	8	2	20	20	18 0.40	1.53	0	0.40	189 P
U37122_at	9	2	20	20	17 0.45	1.45	0	0.45	188 P
M37245_at	10	1	20	20	18 0.50	1.81	0	0.10.0	186 P
U34962_at	8	1	20	20	18 0.45	1.53	0	0.90	186 P
M84556_at	10	3	20	20	18 0.50	1.78	1	0.33	183 P
M31013_at	11	2	20	20	17 0.55	2.34	1	0.55	175 P
U15174_at	7	1	20	20	18 0.35	1.30	0	1.70	173 P
M84856_at	8	1	20	20	18 0.40	1.08	1	0.80	172 P
U00952_at	9	1	20	20	17 0.45	2.14	0	0.90	170 P
U14193_at	8	2	20	20	18 0.40	1.46	0	0.40	170 P
U40343_at	7	1	20	20	18 0.35	1.29	0	0.70	170 P
U02020_at	9	3	20	20	18 0.45	2.42	1	0.30	168 P
U36764_at	10	3	20	20	18 0.50	1.60	1	0.33	167 P
M86667_at	9	3	20	20	18 0.45	1.42	0	0.30	166 P
S69115_at	7	1	20	20	18 0.35	2.01	1	0.70	165 P
M29971_at	8	1	20	20	18 0.40	0.94	0	0.80	165 P
U18937_at	7	2	20	20	18 0.35	1.54	0	1.35	164 P
U31384_at	8	2	20	20	18 0.40	1.12	0	0.40	161 P
S83364_at	9	2	20	20	18 0.45	1.55	0	0.45	159 P
U64778_at	9	3	20	20	18 0.45	1.93	1	0.30	158 P
U03486_at	7	0	20	20	18 0.35	0.91	0	Inf	158 P
M74002_at	7	1	20	20	18 0.35	1.06	0	0.70	157 P
U20325_at	7	2	20	20	18 0.35	1.74	1	0.35	157 P
M80629_at	11	1	20	20	18 0.55	1.58	0	0.11.0	156 P
U20582_at	7	1	20	20	18 0.35	1.01	0	0.70	154 P
U27185_at	9	2	20	20	18 0.45	1.57	0	0.45	152 P
U57721_at	10	1	20	20	18 0.50	2.47	1	0.10.0	150 P
M34423_at	8	1	20	20	18 0.40	1.03	0	0.80	149 P
U47742_at	8	1	20	20	17 0.40	1.12	0	0.80	148 P
U34252_at	10	3	20	20	18 0.50	2.26	2	0.33	148 P
U30899_at	9	3	20	20	17 0.45	1.48	0	0.30	146 P
U53446_at	9	2	20	20	18 0.45	1.43	0	0.45	145 P
S81419_at	7	2	20	20	18 0.35	1.38	0	0.35	143 P
U31383_at	9	3	20	20	18 0.45	1.62	1	0.30	142 P
U29860_at	8	2	20	20	18 0.40	1.47	0	0.40	139 P
M58603_at	8	2	20	20	18 0.40	1.01	0	0.40	138 P
M83425_at	9	1	20	20	18 0.45	1.39	0	0.90	137 P
U21049_at	9	1	20	20	18 0.45	1.31	0	0.90	130 P
U58919_at	9	2	20	20	18 0.45	1.33	0	0.45	128 P
S76965_at	8	1	20	20	18 0.40	2.11	0	0.80	123 P
M28879_at	9	2	20	20	18 0.45	1.50	2	0.45	122 P
U15782_at	7	2	20	20	18 0.35	1.53	1	0.35	122 P
M85276_at	8	2	20	20	18 0.40	0.90	0	0.40	120 P
U03888_at	8	1	20	20	18 0.40	1.65	0	0.80	116 P
U28249_at	7	1	20	20	18 0.35	1.69	1	0.70	115 P
U08316_at	9	3	20	20	18 0.45	1.62	0	0.30	113 P
U07158_at	8	2	20	20	18 0.40	1.19	1	1.40	111 P
U40366_ma1_at	9	2	20	20	18 0.45	1.75	0	1.45	111 P

Side 4

Normal urothelium B									
U49352_at	12	3	20	20	18 0.60	2.61	2	0 4.0	111 P
U59423_at	7	2	20	20	18 0.35	1.31	0	0 3.5	107 P
M65131_ma1_at	7	1	20	20	18 0.35	1.23	0	0 7.0	102 P
U09412_at	8	2	20	20	18 0.40	1.05	0	0 4.0	98 P
U50928_at	11	1	20	20	18 0.55	1.92	1	1 11.0	98 P
U49114_at	10	3	20	20	18 0.50	1.51	1	0 3.3	96 P
U02632_at	9	2	20	20	18 0.45	1.22	0	0 4.5	90 P
U19345_at	7	1	20	20	18 0.35	1.53	0	0 7.0	87 P
U53003_at	9	3	20	20	18 0.45	1.78	1	0 3.0	82 P
U13816_at	9	3	20	20	18 0.45	1.45	2	1 3.0	78 P
U47054_at	7	2	20	20	18 0.35	1.58	2	0 3.5	78 P
M23161_at	8	1	20	20	18 0.40	1.14	0	0 8.0	77 P
M90696_at	9	1	20	20	18 0.45	1.46	2	0 8.0	76 P
U46752_at	8	2	20	20	18 0.40	1.14	0	0 4.0	76 P
U03058_at	7	2	20	20	18 0.35	1.44	2	0 3.5	70 P
U28386_at	9	2	20	20	18 0.45	1.66	1	0 4.5	69 P
U55766_at	7	1	20	20	18 0.35	0.96	0	1 7.0	59 P
U09367_at	8	2	20	20	18 0.40	0.92	0	0 4.0	67 P
U31116_at	7	2	20	20	18 0.35	1.42	1	0 3.5	67 P
U35735_at	7	1	20	20	18 0.35	1.17	0	0 7.0	65 P
U05875_at	7	2	20	20	18 0.35	1.52	0	0 3.5	37 P

Gene Name	Positive			Negative			Pairs	Normal urothelium C					Avg Diff	Abs Call
	Pos	Av	Pos	Neg	Pos	Av		PM Exces	MM Exces	Pos/Neg				
hurr_atu_at	69		0	69	69	67	1.00	7.20	9	0	Inf	22212	P	
Z12882_at	18		0	20	20	18	0.90	7.43	5	0	Inf	11237	P	
X56932_at	20		0	20	20	18	1.00	8.65	9	0	Inf	8427	P	
Z70759_at	20		0	20	20	18	1.00	8.49	8	0	Inf	8169	P	
X69150_at	19		0	20	20	18	0.95	7.61	8	0	Inf	6897	P	
X15940_at	19		0	20	20	18	0.95	7.00	4	0	Inf	5994	P	
X06817_at	20		0	20	20	18	1.00	6.37	1	0	Inf	5392	P	
X03342_at	20		0	20	20	18	1.00	7.66	5	0	Inf	5147	P	
AFFX-CreX-3_at	19		0	20	20	18	0.95	8.47	6	0	Inf	4809	P	
X17206_at	19		0	20	20	18	0.95	7.56	6	0	Inf	4634	P	
X64707_at	15		0	20	20	18	0.75	6.10	3	0	Inf	4230	P	
Z23090_at	17		0	20	20	18	0.85	5.02	0	0	Inf	4116	P	
X62691_at	20		0	20	20	18	1.00	7.40	3	0	Inf	4105	P	
X65814_at	20		0	20	20	18	1.00	7.02	2	0	Inf	4027	P	
AB002533_at	19		0	20	20	18	0.95	6.88	4	0	Inf	4012	P	
X16064_at	17		0	20	20	18	0.85	7.60	4	0	Inf	3795	P	
X63527_at	20		0	20	20	18	1.00	7.94	9	0	Inf	3755	P	
X55954_at	20		0	20	20	18	1.00	7.24	4	0	Inf	3744	P	
AFFX-CreX-5_at	20		0	20	20	18	1.00	8.02	5	0	Inf	3538	P	
X80822_at	18		0	20	20	18	0.90	5.48	0	0	Inf	3471	P	
X67247_ma1_at	20		0	20	20	17	1.00	8.00	6	0	Inf	3402	P	
Z26876_at	19		0	20	20	18	0.95	7.54	5	0	Inf	3163	P	
X73460_at	19		0	20	20	18	0.95	6.44	4	0	Inf	3009	P	
X53777_at	18	1	0	20	20	18	0.90	7.48	6	0	18.0	2851	P	
X78234_at	20		0	20	20	16	1.00	7.48	3	0	Inf	2843	P	
AFFX-HSAC07X00351_3_at	19		0	20	20	18	0.95	6.48	2	0	Inf	2664	P	
X69391_at	20		0	20	20	18	1.00	6.86	4	0	Inf	2656	P	
AFFX-BioDn-3_at	18		0	20	20	18	0.90	5.07	1	0	15.0	2613	P	
Z28407_at	15	1	0	20	20	18	0.75	4.43	1	0	15.0	2557	P	
AFFX-HUMGAPDH/M33197_3_a	19		0	20	20	17	0.95	5.41	0	0	Inf	2535	P	
U76027_rna3_at	18	2	0	20	20	18	0.90	7.15	4	0	9.0	2430	P	
Z25749_ma1_at	16	1	0	20	20	16	0.80	5.44	2	0	16.0	2348	P	
X00274_at	20		0	20	20	16	1.00	8.13	7	0	Inf	2334	P	
X56997_rna1_at	19		0	20	20	18	0.95	5.12	2	0	Inf	2279	P	
Y00705_at	18		0	20	20	18	0.90	7.34	5	0	Inf	2124	P	
:55715_at	17		0	20	20	18	0.85	5.96	2	0	Inf	1884	P	
07755_at	18		0	20	20	18	0.80	6.05	0	0	Inf	1877	P	
52866_at	15	2	0	20	20	17	0.75	5.36	2	0	7.5	1485	P	
:52851_rna1_at	20		0	20	20	18	1.00	6.46	1	0	Inf	1384	P	
:15183_at	17	2	0	20	20	18	0.85	5.76	2	1	8.5	1273	P	
X83036_at	16		0	20	20	18	0.80	5.04	3	0	Inf	1232	P	
X95404_at	14		0	20	20	18	0.70	4.70	2	0	Inf	1170	P	
X57959_at	19		0	20	20	17	0.95	7.19	3	0	Inf	1125	P	
X15341_at	19		0	20	20	18	0.95	6.40	0	0	Inf	1071	P	
AFFX-HSAC07X00351_M_at	16	1	0	20	20	18	0.80	4.07	0	0	16.0	1036	P	
Y00433_at	14		0	20	20	18	0.70	4.15	0	0	Inf	1027	P	
X60489_at	17		0	20	20	18	0.85	5.73	2	0	Inf	996	P	
U90915_at	17		0	20	20	18	0.85	5.47	2	0	Inf	988	P	
X16560_at	18	1	0	20	20	18	0.90	6.30	4	0	18.0	983	P	
X16832_at	16		0	20	20	18	0.80	5.03	1	0	Inf	971	P	
X80909_at	17		0	20	20	18	0.85	5.63	1	0	Inf	939	P	

Side 1

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[illegible]

Normal urothelium C										
L10413_at	10	0	20	20	18 0.50	2.06	0	0	Inf	206 P
U68566_at	9	2	20	20	18 0.45	1.55	0	0	4.5	203 P
U90716_at	11	2	20	20	18 0.55	3.01	3	3	15.5	203 P
X83618_at	12	1	20	20	18 0.60	1.90	0	0	12.0	202 P
X83425_at	9	2	20	20	18 0.45	1.86	0	0	4.5	201 P
X12794_at	8	1	20	20	18 0.45	1.47	0	0	9.0	187 P
X60036_at	14	2	20	20	18 0.70	2.41	0	0	17.0	186 P
X67325_at	10	2	20	20	18 0.50	2.46	0	0	5.0	194 P
U68142_at	11	1	20	20	18 0.55	2.42	0	0	11.0	183 P
X52730_rna1_at	8	1	20	20	18 0.40	1.28	0	0	8.0	182 P
X57346_at	16	0	20	20	17 0.80	3.12	0	0	Inf	191 P
X74795_at	9	2	20	20	17 0.45	1.61	0	0	4.5	190 P
X62456_at	13	2	20	20	18 0.65	3.07	0	0	6.5	190 P
X03218_at	16	0	20	20	17 0.80	3.40	0	0	Inf	190 P
U79254_at	14	0	20	20	18 0.70	2.90	0	0	Inf	188 P
X66401_cds1_at	11	2	20	20	18 0.55	3.24	1	1	5.5	188 P
Z35093_at	10	0	20	20	18 0.50	2.48	0	0	Inf	188 P
X54304_at	10	0	20	20	18 0.50	2.85	1	1	0	187 P
X95986_at	12	1	20	20	18 0.60	2.55	1	1	12.0	187 P
X70476_at	13	2	20	20	18 0.65	3.26	1	1	6.5	186 P
X58733_rna1_at	7	1	20	20	18 0.35	1.53	0	0	7.0	185 P
U73379_at	11	2	20	20	17 0.55	1.92	0	0	5.5	181 P
U77398_at	10	2	20	20	18 0.50	2.09	0	0	5.0	180 P
X17620_at	7	1	20	20	18 0.35	1.16	0	0	7.0	178 P
X69910_at	13	2	20	20	18 0.65	2.25	0	0	6.5	176 P
X98459_at	8	1	20	20	18 0.40	1.40	0	0	8.0	178 P
X99920_at	12	1	20	20	18 0.60	1.52	0	0	12.0	176 P
X15414_at	12	0	20	20	17 0.60	2.21	0	0	Inf	174 P
Z29505_at	15	1	20	20	18 0.75	3.40	1	1	15.0	174 P
Z37986_at	11	2	20	20	18 0.55	1.92	0	0	5.5	174 P
Z19574_rna1_at	14	0	20	20	17 0.70	2.84	0	0	Inf	173 P
U76625_at	7	0	20	20	18 0.35	1.45	0	0	Inf	172 P
X59434_at	10	2	20	20	18 0.50	1.34	0	0	5.0	172 P
Y11681_at	9	1	20	20	18 0.45	1.54	0	0	9.0	172 P
X98209_at	9	2	20	20	18 0.45	1.65	0	0	4.5	170 P
U72515_at	7	1	20	20	18 0.35	1.29	0	0	7.0	168 P
U70860_at	11	2	20	20	17 0.55	1.80	0	0	5.5	160 P
X61970_at	11	2	20	20	18 0.55	2.56	0	0	5.5	159 P
U94592_at	13	2	20	20	17 0.65	2.02	0	0	6.5	158 P
X62078_at	12	1	20	20	18 0.60	1.64	0	0	12.0	157 P
U82010_rna1_at	11	1	20	20	18 0.55	2.44	0	0	11.0	156 P
X63422_at	10	1	20	20	18 0.50	2.41	0	0	10.0	156 P
X72964_at	11	1	20	20	18 0.55	1.79	0	0	11.0	153 P
X76228_at	11	3	20	20	18 0.55	2.46	1	1	3.7	153 P
U83246_at	8	2	20	20	18 0.40	1.04	0	0	4.0	152 P
U78266_at	7	1	20	20	18 0.35	1.07	0	0	7.0	148 P
U90547_at	9	0	20	20	17 0.45	2.01	0	0	Inf	148 P
X97074_at	8	0	20	20	18 0.40	1.27	0	0	Inf	148 P
D50405_at	9	1	20	20	18 0.45	1.59	0	0	9.0	148 P
U93237_rna2_at	10	1	20	20	18 0.50	1.70	0	0	10.0	146 P
X67237_at	9	1	20	20	18 0.45	1.45	0	0	9.0	146 P
Z14244_at	13	2	20	20	18 0.65	2.65	1	1	6.5	146 P
X74295_at	10	1	20	20	18 0.50	1.75	0	0	10.0	145 P

Side 4

X89750_at	14	0	20	20	18.070	3.67	1	0	Inf	145 P
U68233_at	8	2	20	20	18.040	1.71	0	0	0.40	144 P
U72517_at	9	2	20	20	18.045	1.34	0	0	0.45	144 P
X03034_at	10	0	20	20	18.050	2.02	0	0	0 Inf	143 P
U70735_at	12	0	20	20	18.060	1.96	0	0	0 Inf	143 P
U76524_at	10	2	20	20	18.050	1.67	0	0	0.50	138 P
X57398_at	9	1	20	20	18.045	2.09	0	0	0.90	137 P
U87459_at	7	2	20	20	18.035	1.33	0	0	0.35	137 P
X04366_at	10	3	20	20	18.050	2.02	0	0	0.33	137 P
Y00815_at	10	1	20	20	18.050	2.29	0	0	0.10.0	135 P
AFFX-HUMISGF3A/M87035_3_a	10	1	20	20	18.050	1.69	0	0	0.10.0	135 P
U79287_at	8	1	20	20	18.040	1.91	0	0	0.80	135 P
X12451_at	13	0	20	20	17.065	2.96	1	0	0 Inf	135 P
Z49099_at	8	1	20	20	18.040	1.69	1	0	0.80	134 P
X05409_at	11	2	20	20	18.055	1.38	0	0	0.55	133 P
X69433_at	8	2	20	20	18.040	1.33	0	0	0.40	133 P
U75988_at	8	1	20	20	18.040	1.15	0	0	0.80	132 P
L11068_at	9	2	20	20	18.045	1.08	0	0	0.45	132 P
X62744_at	11	3	20	20	17.055	1.93	0	0	0.37	131 P
U89338_cds1_at	8	1	20	20	18.040	1.73	0	0	0.80	130 P
U80807_at	9	2	20	20	18.045	1.38	0	0	0.45	130 P
X02434_at	9	0	20	20	17.045	1.38	0	0	0 Inf	130 P
X02200_at	9	3	20	20	18.045	2.01	1	0	0.30	129 P
X65373_at	10	2	20	20	18.050	1.40	1	0	0.50	129 P
Z47727_at	9	0	20	20	18.045	1.98	0	0	0 Inf	129 P
X71129_at	9	1	20	20	17.045	1.45	0	0	0.90	127 P
U85193_at	10	1	20	20	18.050	2.01	0	0	0.10.0	126 P
X78534_at	14	1	20	20	18.070	3.70	0	0	1 14.0	125 P
Z71460_at	8	2	20	20	18.040	1.42	0	0	0.40	125 P
U81556_at	8	1	20	20	17.040	1.50	0	0	0.80	124 P
U68063_at	10	1	20	20	18.050	3.10	2	0	0.10.0	123 P
X82885_at	7	0	20	20	18.035	1.31	0	0	0 Inf	123 P
X74262_at	14	2	20	20	18.070	3.68	3	0	0.70	120 P
Z58281_at	7	1	20	20	18.035	1.17	0	0	0.70	120 P
X77794_at	16	2	20	20	17.080	3.79	1	0	0.80	119 P
X54232_at	8	2	20	20	18.040	1.05	0	0	0.40	118 P
AFFX-Blob3_3_at	9	0	20	20	17.045	1.44	0	0	0 Inf	118 P
U78793_at	8	2	20	20	16.040	1.81	0	0	0.40	115 P
X60692_at	10	1	20	20	18.050	2.36	1	0	0.10.0	115 P
X98311_at	9	1	20	20	18.045	1.43	0	0	0.80	113 P
X04612_at	8	2	20	20	18.040	0.98	0	0	0.40	111 P
X99728_at	10	3	20	20	18.050	1.80	0	0	0.33	111 P
X58405_at	11	2	20	20	18.055	1.92	0	0	0.55	110 P
X92886_at	12	1	20	20	18.045	1.52	0	0	0.12.0	109 P
X76848_at	9	3	20	20	17.045	1.52	0	0	0.30	108 P
X15187_at	13	1	20	20	18.065	4.02	1	0	0.13.0	107 P
U89278_at	9	2	20	20	17.045	2.15	0	0	0.45	106 P
X62055_at	8	2	20	20	17.040	0.91	0	0	0.40	105 P
X68277_at	9	1	20	20	17.045	1.53	0	0	0.90	105 P
X74008_at	11	2	20	20	18.055	1.64	0	0	0.55	105 P
U78556_at	11	1	20	20	17.055	2.21	0	0	0.11.0	104 P
U89336_cds3_at	9	1	20	20	18.045	1.41	0	0	0.90	104 P
	9	0	20	20	17.045	1.26	0	0	0 Inf	104 P

Side 5

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X69141_at	12	2	20	20	17.060	2.35	0	0.60	104 P
X78180_at	8	1	20	20	18.040	1.39	0	0.80	104 P
U81932_at	9	1	20	20	17.045	1.82	0	0.90	103 P
Z69720_at	9	2	20	20	17.045	1.15	0	0.45	101 P
U91930_at	11	1	20	20	18.055	2.15	0	0.11.0	100 P
V01512_mna1_at	10	1	20	20	18.050	1.73	0	0.10.0	100 P
Z48042_at	10	2	20	20	18.050	1.74	0	0.50	99 P
X75862_at	8	1	20	20	18.040	1.50	0	0.80	98 P
X84740_at	7	2	20	20	18.035	1.33	0	0.35	98 P
U78241_at	10	3	20	20	17.050	2.01	0	0.33	97 P
X98411_at	8	1	20	20	18.040	1.35	0	0.80	97 P
X79781_at	11	0	20	20	18.055	1.58	0	0.1nf	96 P
U85932_at	7	0	20	20	17.035	1.22	0	0.1nf	95 P
X75304_at	7	0	20	20	18.035	1.21	0	0.1nf	95 P
Z37166_at	10	1	20	20	17.050	1.32	0	0.10.0	95 P
X81123_at	12	1	20	20	17.060	2.74	1	0.12.0	94 P
U80426_at	8	0	20	20	18.045	1.86	1	0.1nf	93 P
X94754_at	9	0	20	20	18.045	1.46	0	0.1nf	93 P
X99585_at	8	2	20	20	18.045	1.19	0	0.45	93 P
X12781_at	9	3	20	20	18.045	1.69	1	0.30	92 P
U86802_at	8	2	20	20	18.040	1.23	0	0.40	91 P
Z47087_at	12	1	20	20	17.060	1.95	0	0.12.0	89 P
U67963_at	7	2	20	20	18.035	1.81	0	0.35	87 P
Z15114_at	10	2	20	20	18.050	1.12	0	0.50	87 P
AFFX-HUMRGE/M10098_5_at	10	1	20	20	17.050	2.34	1	0.10.0	85 P
X57522_at	8	2	20	20	18.040	1.13	1	0.40	85 P
Y08915_at	9	2	20	20	18.045	0.93	0	1.45	85 P
U88629_at	9	2	20	20	17.045	1.88	0	0.45	84 P
X61100_mna1_at	10	0	20	20	18.050	2.11	0	0.1nf	84 P
X91247_at	10	2	20	20	18.050	1.59	0	0.50	84 P
Y07867_at	9	3	20	20	18.045	1.70	0	0.30	84 P
X76538_at	7	2	20	20	18.035	1.88	0	0.35	82 P
X82103_at	10	1	20	20	18.050	1.68	0	0.10.0	82 P
U72514_at	8	2	20	20	18.040	1.89	0	0.40	81 P
X82153_at	13	1	20	20	18.065	2.48	0	0.13.0	81 P
X06614_at	6	2	20	20	18.040	1.41	1	0.40	80 P
Z68747_at	7	2	20	20	18.035	1.32	0	0.35	80 P
U72508_at	7	0	20	20	18.035	1.06	0	0.1nf	79 P
X07024_at	9	2	20	20	18.045	2.76	2	0.45	78 P
Y13115_at	9	2	20	20	18.045	1.27	0	0.45	78 P
U68645_at	11	2	20	20	18.035	1.57	1	0.35	76 P
X63469_at	7	3	20	20	18.055	1.93	0	0.37	75 P
X76057_at	8	1	20	20	18.040	0.98	0	0.80	75 P
Z29083_at	7	1	20	20	17.035	1.39	0	0.70	73 P
X80497_at	8	2	20	20	18.040	1.82	1	0.40	72 P
Z22551_at	9	2	20	20	18.045	1.99	0	0.45	72 P
U77643_at	8	2	20	20	18.040	0.96	0	0.40	71 P
U80919_at	13	3	20	20	18.065	2.64	3	1.43	71 P
X02530_at	7	1	20	20	18.035	1.63	0	0.70	71 P
X05276_at	11	3	20	20	18.055	1.54	1	0.37	71 P
X67155_at	10	3	20	20	18.050	1.51	1	0.33	71 P
U83463_at	11	1	20	20	17.055	2.14	1	0.11.0	69 P
Z70219_at	7	1	20	20	18.035	1.77	0	0.70	69 P

Normal urothellum C									
	8	2	20	20	17.040	1.14	0	0.40	68 P
X73079_at	8	1	20	20	18.040	1.83	1	0.80	68 P
X724725_at	8	3	20	20	18.045	1.96	0	1.30	68 P
X36531_at	10	1	20	20	18.050	1.50	0	0.100	87 P
X84708_at	8	2	20	20	18.040	1.27	0	0.40	66 P
X5740_mn2_at	8	2	20	20	18.045	2.08	1	0.45	66 P
X80910_at	9	1	20	20	18.040	1.88	1	0.80	65 P
X83461_at	8	0	20	20	17.045	2.85	1	0.1nf	65 P
Y10506_at	9	2	20	20	17.040	1.14	0	0.40	65 P
X235491_at	8	2	20	20	18.045	1.85	1	0.1nf	64 P
X81003_at	9	0	20	20	17.050	1.80	1	0.50	63 P
X04287_at	10	2	20	20	17.045	1.90	1	0.80	63 P
X63753_at	9	1	20	20	18.055	2.73	2	0.55	62 P
U79274_at	11	2	20	20	17.040	1.49	1	0.40	61 P
U96629_mn2_at	8	2	20	20	18.055	2.01	2	0.37	60 P
X83368_at	11	3	20	20	18.035	0.92	0	0.1nf	59 P
X50853_at	7	0	20	20	18.040	1.43	0	0.40	58 P
AFFX-M27830_5_at	8	2	20	20	18.045	1.76	1	0.30	58 P
X83378_at	8	3	20	20	18.040	0.98	0	0.40	57 P
U79265_at	9	3	20	20	18.045	1.57	1	0.30	57 P
X02612_at	11	3	20	20	18.055	2.67	2	0.37	56 P
X96586_at	7	1	20	20	17.035	1.32	1	0.70	56 P
X98283_at	7	1	20	20	18.035	0.92	0	0.70	55 P
U66469_at	8	0	20	20	18.040	1.03	0	0.1nf	55 P
X54941_at	8	0	20	20	17.045	1.42	0	0.90	54 P
U78313_at	9	1	20	20	18.045	1.70	1	1.80	54 P
U90651_at	9	1	20	20	17.050	1.71	0	0.33	52 P
X65873_at	10	3	20	20	18.045	1.05	0	0.45	52 P
D08660_at	9	2	20	20	18.040	1.56	0	0.80	51 P
X92098_at	8	1	20	20	18.035	1.11	0	1.70	49 P
X88742_at	7	1	20	20	18.050	2.18	3	0.100	49 P
X92396_at	10	1	20	20	18.040	1.44	0	0.40	48 P
X59841_at	8	2	20	20	18.055	2.36	2	0.1nf	48 P
X61116_mn1_at	11	0	20	20	18.045	1.00	1	1.45	48 P
Y12711_at	9	2	20	20	18.045	1.37	0	0.30	47 P
X63679_at	8	3	20	20	18.040	1.84	0	0.40	47 P
X95372_at	8	2	20	20	18.040	1.73	0	0.40	47 P
X87212_at	8	2	20	20	18.040	1.22	1	0.40	46 P
X76732_at	8	2	20	20	18.045	2.45	2	0.90	45 P
U70242_at	8	1	20	20	17.040	1.90	0	0.40	45 P
U79273_at	8	2	20	20	18.040	1.59	1	0.40	43 P
X02596_at	8	2	20	20	18.040	1.38	0	1.80	43 P
X53586_mn1_at	8	1	20	20	18.045	1.19	0	0.45	40 P
U66669_at	10	2	20	20	18.050	1.39	0	0.50	40 P
U77129_at	9	2	20	20	18.045	2.24	2	0.90	39 P
X84194_at	9	1	20	20	18.045	1.48	0	0.90	38 P
Z24724_at	8	1	20	20	17.040	0.99	0	1.80	37 P
U73191_at	8	1	20	20	18.045	0.93	0	0.45	36 P
U89336_ctb6_at	8	2	20	20	18.040	1.33	0	0.80	36 P
X82207_at	7	1	20	20	18.035	1.25	1	0.70	36 P
X96752_at	9	2	20	20	18.045	1.39	1	0.45	36 P
X97544_at	9	0	20	20	18.045	2.38	2	0.1nf	36 P
Y07701_at	6	0	20	20	18.040	1.16	0	0.1nf	36 P

Side 7

	Normal urothelium C										
U79298_at	11	3	20	20	17 0.55	1.62	0	0.37	35 P		
U91327_at	10	3	20	20	18 0.50	1.46	0	0.33	34 P		
X06290_at	7	1	20	20	17 0.35	1.24	0	0.70	34 P		
Y00571_ma1_at	12	4	20	20	18 0.60	1.83	1	0.30	33 P		
X15949_at	9	1	20	20	18 0.45	1.90	0	0.90	33 P		
X54925_at	9	1	20	20	18 0.45	2.36	1	0.90	33 P		
X64228_at	9	3	20	20	18 0.45	2.19	1	0.30	33 P		
U89355_at	7	1	20	20	18 0.35	1.80	2	0.70	27 P		
X67337_at	2	20	20	20	18 0.50	2.52	2	0.50	25 P		
Y09815_at	10	3	20	20	18 0.45	1.54	0	0.30	25 P		
J75679_at	8	2	20	20	18 0.40	2.29	2	1.40	24 P		
X52011_at	7	1	20	20	18 0.35	1.01	0	0.70	23 P		
Y08991_at	9	2	20	20	18 0.45	2.10	3	0.45	22 P		
Z48511_at	7	2	20	20	18 0.35	1.36	2	0.35	22 P		

Normal urothelium D

Gene name	Pos	Fractl	Log Avg	Pos/Neg	Avg Diff	Abs Call
hum_ali_at	0.93	4.78	19333 P	Under	11710 P	11710 P
LO4483_s_at	1.00	6.39	8316 P	Under	7387 P	7387 P
M63438_s_at	0.94	5.38	7240 P	Under	7095 P	7095 P
AFFX-CreX-3_at	1.00	7.08	6543 P	Under	6479 P	6479 P
M14199_s_at	1.00	6.11	6165 P	Under	6034 P	6034 P
M31520_mna1_s_at	1.00	7.41	5719 P	Under	5581 P	5581 P
D13413_mna1_s_at	0.94	5.13	5284 P	Under	5188 P	5188 P
J04617_s_at	0.94	6.13	5075 P	Under	4813 P	4813 P
J00105_s_at	1.00	8.49	4370 P	Under	4215 P	4215 P
HG2815-HT4023_s_at	0.95	5.52	4111 P	Under	4088 P	4088 P
AFFX-CreX-5_at	1.00	7.24	3875 P	Under	3815 P	3815 P
U06155_s_at	0.86	5.26	3718 P	Under	3615 P	3615 P
HG1428-HT1428_s_at	0.90	6.57	3097 P	Under	3076 P	3076 P
M10277_s_at	0.90	5.39	2957 P	Under	2844 P	2844 P
X52426_s_at	0.95	4.65	2759 P	Under	2730 P	2730 P
M25079_s_at	0.75	3.56	2613 P	Under	2532 P	2532 P
HG2815-HT2931_at	1.00	4.67	2448 P	Under	2419 P	2419 P
X57351_s_at	1.00	6.06	2332 P	Under	2281 P	2281 P
AFFX-HSAC07/X00351_3_at	0.95	4.89	2172 P	Under	2127 P	2127 P
U43901_mna1_s_at	0.90	4.89	1884 P	Under	1837 P	1837 P
M36072_at	0.75	3.70	1637 P	Under	1577 P	1577 P
AFFX-HUMGAPDH/M33197_3_a	0.95	5.10	1620 P	Under	1517 P	1517 P
V00594_s_at	1.00	6.24	1610 P	Under	1529 P	1529 P
X69654_at	0.95	6.24	150	Under	1411 P	1411 P
S71043_mna1_s_at	0.80	3.63	1371 P	Under	1315 P	1315 P
D48824_s_at	1.00	5.68	1248 P	Under	1184 P	1184 P
Z49148_s_at	1.00	5.41	1177 P	Under	1117 P	1117 P
X17093_at	0.60	2.80	1084 P	Under	1037 P	1037 P
S82297_at	0.95	4.02	984 P	Under	937 P	937 P
AFFX-BioDn-3_at	0.75	3.55	884 P	Under	837 P	837 P
U68105_s_at	0.95	7.09	784 P	Under	737 P	737 P
M34516_at	1.00	3.14	684 P	Under	637 P	637 P
M65409_s_at	0.85	5.66	584 P	Under	537 P	537 P
X98482_f_at	0.33	1.36	484 P	Under	437 P	437 P
X03589_s_at	1.00	0.82	384 P	Under	337 P	337 P
HG5598-HT658_f_at	0.73	3.32	284 P	Under	237 P	237 P
X01677_f_at	0.85	4.02	184 P	Under	137 P	137 P
M26708_s_at	1.00	5.58	84 P	Under	37 P	37 P
D32128_f_at	0.85	5.02	17 P	Under	17 P	17 P
M14483_mna1_s_at	0.80	4.11	17 P	Under	17 P	17 P
X51345_at	0.75	4.45	17 P	Under	17 P	17 P
HG3991-HT4261_r_at	0.45	2.24	17 P	Under	17 P	17 P
M34516_f_at	0.91	4.72	17 P	Under	17 P	17 P
X00351_f_at	0.90	5.53	17 P	Under	17 P	17 P
D86874_at	0.85	3.82	17 P	Under	17 P	17 P
AFFX-HSAC07/X00351_M_at	0.75	3.80	17 P	Under	17 P	17 P
HG3342-HT3519_s_at	0.89	5.01	17 P	Under	17 P	17 P
M55998_s_at	0.65	5.62	17 P	Under	17 P	17 P
HG3431-HT3616_s_at	0.85	6.18	17 P	Under	17 P	17 P

Normal urothellum D

HG417-HT417_s_at	0.90	5.16	Under	1481 P
HG2147-HT2217_at	0.83	1.76	5.0	1428 P
M33600_f_at	0.80	3.73	Under	1395 P
X99133_at	0.80	2.86	12.0	1351 P
U57341_f_at	1.00	4.38	Under	1344 P
S54005_s_at	0.80	4.83	Under	1309 P
J04152_ma1_s_at	0.90	5.26	18.0	1281 P
M13560_s_at	0.80	4.20	16.0	1286 P
M24485_s_at	0.65	3.17	Under	1234 P
HG3597-HT3800_f_at	0.80	4.54	18.0	1146 P
M12125_at	0.65	3.02	13.0	1144 P
J03801_f_at	0.90	5.19	Under	1137 P
HG1980-HT2023_at	0.45	2.42	Under	1132 P
M87789_s_at	0.75	2.57	15.0	1078 P
X04347_s_at	0.90	6.03	Under	1076 P
X14008_ma1_f_at	0.75	4.95	15.0	1072 P
S75256_s_at	0.80	3.92	16.0	1089 P
M94880_f_at	0.50	2.24	Under	1061 P
M19311_s_at	0.81	5.08	13.0	1040 P
HG1515-HT1515_f_at	0.75	4.84	15.0	1005 P
AFFX-HSAC07X00351_5_at	0.80	3.09	16.0	958 P
J03077_s_at	0.65	3.77	13.0	925 P
X12671_ma1_at	0.90	4.19	Under	917 P
M14328_s_at	0.75	3.54	7.5	885 P
X74929_s_at	0.65	2.81	Under	869 P
L11672_at	0.50	2.21	Under	855 P
U05861_at	0.70	3.82	14.0	850 P
M26730_s_at	0.85	4.45	8.5	838 P
Z19554_s_at	0.78	4.15	14.0	827 P
AFFX-HUMGAPDH33197_M_0.60	0.75	2.75	6.0	802 P
M19045_f_at	0.75	5.50	15.0	794 P
AFFX-HSAC07X00351_3_at	0.75	3.50	Under	779 P
HG2815-HT2931_s_at	0.93	4.96	Under	767 P
U70439_s_at	0.75	4.30	Under	766 P
X56681_s_at	0.65	2.68	6.5	766 P
Z48501_s_at	0.74	3.63	Under	748 P
X12876_s_at	0.70	4.75	14.0	745 P
HG3576-HT3779_f_at	0.65	2.88	6.5	734 P
Z69043_s_at	0.70	3.45	7.0	722 P
HG2915-HT3059_f_at	0.65	2.34	Under	720 P
M11313_s_at	0.65	3.19	13.0	717 P
M26311_s_at	0.63	2.85	12.0	686 P
AFFX-BioOn-5_at	0.80	3.30	16.0	683 P
HG2917-HT3061_f_at	0.80	2.11	Under	663 P
U04241_at	0.45	2.22	9.0	659 P
D17793_at	0.70	4.00	14.0	650 P
M62403_s_at	0.65	2.40	Under	648 P
HG3236-HT3413_f_at	0.50	2.18	10.0	635 P
L33075_at	0.55	2.57	Under	634 P
X57809_s_at	0.58	2.03	Under	629 P
Z49107_s_at	0.45	1.28	4.5	623 P

Normal urothellum D

AFFX-HUMGAPDHUM33187_s_a0.75	4.14	15.0	622 P
U48705_maf_s_at	2.63	3.7	610 P
X03068_f_at	2.28	24.0	606 P
L02326_f_at	2.32	3.7	586 P
AJ000099_s_at	2.08	9.0	546 P
M21142_caf52_s_at	2.18	3.3	546 P
Z15115_at	3.51	Under	543 P
X58841_at	2.13	10.0	540 P
AFFX-BioC-5_at	2.87	6.5	537 P
L06209_s_at	3.77	Under	537 P
HG4264-HT4534_s_at	4.39	Under	530 P
V00599_a_at	2.24	5.5	528 P
X04854_s_at	2.30	4.0	488 P
L40397_at	2.78	14.0	487 P
M86995_s_at	4.0	4.0	470 P
AFFX-BioC-3_at	2.22	6.0	459 P
M83667_maf_s_at	3.14	15.0	444 P
D00749_s_at	1.30	4.5	438 P
U88898_f_at	1.59	Under	422 P
HG1322-HT15143_s_at	3.87	14.0	415 P
U72649_at	2.87	13.0	412 P
U00947_s_at	4.51	Under	403 P
M16336_s_at	2.18	5.5	401 P
X04470_s_at	3.37	Under	398 P
M85292_s_at	2.95	Under	394 P
HG688-HT688_f_at	2.11	12.0	390 P
HG371-HT26388_s_at	2.30	7.0	380 P
M16342_at	2.05	Under	374 P
X58072_at	2.50	Under	373 P
X57351_at	2.13	4.0	369 P
M89013_at	2.79	12.0	368 P
Z28491_s_at	3.48	7.5	361 P
M30448_s_at	2.08	5.5	357 P
L49380_at	1.37	4.5	354 P
U80552_s_at	3.90	Under	347 P
HG3076-HT3238_s_at	2.99	12.0	346 P
X85116_maf_s_at	2.08	3.7	331 P
D17408_s_at	2.31	10.0	325 P
J02871_s_at	2.46	6.0	319 P
M57466_s_at	2.81	Under	312 P
K02405_f_at	1.30	7.0	309 P
M23323_s_at	1.87	11.0	309 P
L39330_s_at	1.68	Under	307 P
X04526_at	2.22	Under	305 P
Z35402_maf_s_at	3.12	14.0	305 P
Y00264_at	3.15	13.0	302 P
L00389_f_at	1.73	Under	301 P
M12959_s_at	2.34	Under	295 P
X15729_s_at	3.92	7.0	295 P
D78577_s_at	2.40	4.0	291 P
M16276_at	1.87	Under	285 P

Normal urothelium D

J05582_s_at	0.50	1.55	Undef	283 P
U08021_at	0.50	1.84	10.0	275 P
M97935_s_at	0.60	2.49	4.0	273 P
D79208_s_at	0.40	1.26	Undef	270 P
X01703_at	0.65	2.81	Undef	267 P
J04093_s_at	0.70	4.37	Undef	265 P
X17567_s_at	0.45	1.85	3.0	261 P
HG4535-HT4940_s_at	0.35	1.29	7.0	259 P
L24774_s_at	0.45	1.63	4.5	259 P
M58525_s_at	0.40	1.38	8.0	259 P
X14694_s_at	0.50	1.79	5.0	258 P
M37457_at	0.50	1.93	Undef	257 P
U49835_s_at	0.60	2.17	Undef	257 P
X94563_xp12_r_at	0.33	1.35	Undef	255 P
M13690_s_at	0.50	2.07	Undef	252 P
S40719_s_at	0.50	1.63	3.3	251 P
X05130_s_at	0.58	1.95	11.0	247 P
U50079_s_at	0.60	2.55	3.0	243 P
AC002045_xp12_s_at	0.55	2.10	11.0	231 P
M10942_at	0.45	2.13	3.0	228 P
D42040_s_at	0.40	1.08	4.0	224 P
L76517_at	0.35	1.27	7.0	221 P
U32988_s_at	0.40	1.48	8.0	218 P
X52979_ma1_s_at	0.55	2.08	11.0	218 P
X53296_s_at	0.65	2.54	5.5	217 P
X90846_at	0.60	1.90	Undef	214 P
AFFX-HUMISGF3AM97935_3_a	0.65	3.14	Undef	209 P
L05187_at	0.45	1.97	9.0	209 P
X65965_s_at	0.67	2.90	Undef	209 P
S50017_s_at	0.55	2.17	5.5	208 P
X72727_at	0.55	1.95	Undef	204 P
X74874_ma1_s_at	0.45	2.13	9.0	203 P
J03805_s_at	0.50	3.17	9.0	202 P
X55037_s_at	0.55	1.49	3.7	201 P
HG4541-HT4946_s_at	0.61	1.85	3.7	197 P
U78528_s_at	0.50	1.17	Undef	195 P
Z49835_s_at	0.50	3.00	5.0	195 P
U03598_at	0.50	1.84	Undef	191 P
L22524_s_at	0.50	2.89	9.0	190 P
M93851_at	0.60	2.33	Undef	190 P
U38341_ma1_at	0.35	1.33	3.5	188 P
M19267_s_at	0.63	2.37	6.0	186 P
U07806_s_at	0.55	2.51	3.7	185 P
M34996_s_at	0.60	2.17	12.0	184 P
X77588_s_at	0.50	1.90	3.3	184 P
L12711_s_at	0.47	1.69	4.5	181 P
S02447_s_at	0.35	1.11	7.0	180 P
U09587_at	0.65	2.63	6.5	178 P
S69272_s_at	0.45	1.49	3.0	177 P
X62083_s_at	0.50	1.18	5.0	177 P
J03242_s_at	0.35	1.56	7.0	172 P

Normal urothellum D

AB006781_s_at	0.35	1.23	171 P
L42583_f_at	0.50	1.38	169 P
X98296_at	0.35	0.98	169 P
U28014_at	0.60	3.02	169 P
S80437_g_at	0.45	1.55	166 P
S82597_rna1_s_at	0.50	1.67	166 P
U16799_s_at	0.60	2.36	163 P
X57152_rna1_s_at	0.45	1.57	160 P
X07438_s_at	0.63	3.50	159 P
AFFX-HUMRGE/M10088_5_at	0.55	2.14	158 P
D00408_s_at	0.45	1.41	156 P
M28213_s_at	0.65	1.93	156 P
M92843_s_at	0.45	1.62	154 P
Z11899_s_at	0.40	1.32	154 P
X73358_s_at	0.47	1.25	153 P
U77846_rna1_s_at	0.40	1.93	151 P
X05855_s_at	0.53	2.84	143 P
M27394_s_at	0.45	1.60	142 P
U61734_g_at	0.47	1.40	140 P
Z25521_s_at	0.40	1.23	140 P
X83416_s_at	0.55	2.60	139 P
X52022_at	0.45	2.00	138 P
U22431_g_at	0.50	2.19	135 P
HG2090-HT2152_s_at	0.42	1.54	132 P
L14778_s_at	0.58	2.72	132 P
D83174_s_at	0.40	1.41	131 P
M13828_s_at	0.45	1.75	131 P
U41654_at	0.60	1.95	129 P
U61397_s_at	0.45	1.61	129 P
M20867_s_at	0.53	2.56	127 P
Y00767_s_at	0.55	2.37	127 P
Y00451_s_at	0.45	1.77	125 P
L15189_s_at	0.50	2.51	124 P
X06700_s_at	0.50	1.59	124 P
HG2743-HT2846_g_at	0.40	0.91	123 P
Y00097_s_at	0.50	1.46	123 P
D83260_g_at	0.47	1.60	121 P
HG4334-HT4504_s_at	0.35	1.16	120 P
Z47055_s_at	0.35	1.65	120 P
X02761_s_at	0.55	1.65	119 P
X89398_s_at	0.45	0.97	118 P
D78132_s_at	0.60	1.92	117 P
D28473_s_at	0.70	2.85	115 P
S57212_s_at	0.40	1.35	115 P
HG4657-HT4962_f_at	0.60	1.92	114 P
U61276_g_at	0.50	2.19	114 P
U60061_at	0.60	2.43	113 P
J04130_g_at	0.50	1.66	110 P
M63838_s_at	0.45	2.03	110 P
S79219_s_at	0.55	1.48	109 P
U58046_s_at	0.45	2.81	109 P

Normal urothelium D

X03363_s_at	0.35	1.58	3.5	109 P
X76942_s_at	0.60	2.40	6.0	109 P
HG3925-HT14195_at	0.40	1.45	Undef	106 P
M61632_s_at	0.40	1.11	8.0	106 P
U80226_s_at	0.40	1.85	4.0	103 P
X72889_at	0.35	1.53	Undef	103 P
HG3484-HT3678_s_at	0.45	1.66	Undef	99 P
D49372_s_at	0.35	1.28	7.0	97 P
AFFX-MZ7830_5_at	0.40	1.16	Undef	95 P
S68805_at	0.50	1.96	Undef	95 P
M14745_at	0.50	1.09	10.0	94 P
U06155_at	0.50	1.18	Undef	94 P
Z35086_s_at	0.42	2.60	4.0	93 P
U44799_s_at	0.40	1.60	4.0	92 P
X62534_s_at	0.80	2.49	4.0	92 P
M33684_s_at	0.35	1.42	3.5	91 P
U73936_at	0.45	1.01	Undef	90 P
X85137_s_at	0.40	1.80	8.0	90 P
HG1400-HT1400_s_at	0.50	2.62	10.0	89 P
X80530_at	0.55	2.41	3.7	88 P
X92368_at	0.55	2.41	5.5	88 P
D25535_s_at	0.45	1.84	4.5	87 P
HG4593-HT4998_at	0.50	1.39	3.3	86 P
U41740_at	0.45	2.35	8.0	86 P
X12530_s_at	0.42	1.23	Undef	86 P
AFFX-HUMRGE/M10098_M_at	0.45	1.35	4.5	85 P
U26424_at	0.45	2.48	Undef	84 P
X57809_at	0.50	1.27	4.0	84 P
HG210-HT210_s_at	0.60	2.00	8.0	83 P
HG2981-HT3125_s_at	0.50	1.51	5.0	82 P
U30827_s_at	0.50	1.22	5.0	82 P
M34715_at	0.45	1.39	Undef	80 P
D89377_s_at	0.38	0.97	Undef	78 P
L12760_s_at	0.42	1.78	8.0	75 P
M24059_at	0.45	2.05	3.0	75 P
L43579_s_at	0.40	1.48	3.0	74 P
U01691_s_at	0.35	1.37	Undef	74 P
L00634_s_at	0.53	2.30	3.3	71 P
U19495_s_at	0.65	2.98	4.3	71 P
HG2148-HT2218_f_at	0.35	1.33	3.5	70 P
L25931_s_at	0.55	1.99	11.0	69 P
U20536_s_at	0.45	1.79	Undef	69 P
U77846_ma1_at	0.40	1.34	Undef	68 P
U19147_s_at	0.55	3.75	11.0	66 P
L18677_f_at	0.35	1.26	Undef	64 P
M90356_f_at	0.40	0.92	4.0	63 P
D00003_s_at	0.42	1.46	Undef	62 P
AF012024_s_at	0.40	1.35	4.0	60 P
M16652_at	0.50	1.24	Undef	58 P
U09279_at	0.40	2.24	8.0	58 P
L78833_cds1_at	0.40	1.22	8.0	57 P

Normal urothellum D

M24736_s_at	0.45	2.83	Undef	57 P
D63861_s_at	0.65	3.10	4.3	58 P
U26173_s_at	0.40	0.93	4.0	55 P
U53632_at	0.40	1.11	4.0	53 P
X70944_s_at	0.40	1.97	4.0	53 P
X03350_at	0.45	0.99	9.0	52 P
U20938_at	0.45	1.36	3.0	50 P
X01625_at	0.45	1.93	4.5	48 P
HG38-HT4101_s_at	0.33	1.47	3.0	47 P
U47077_at	0.40	1.22	Undef	47 P
X59244_f_at	0.35	1.32	3.5	47 P
X92493_s_at	0.45	2.05	3.0	47 P
U49020_cd52_s_at	0.35	1.59	3.5	46 P
U72938_s_at	0.35	1.32	7.0	45 P
M14758_at	0.35	1.45	3.5	42 P
S76853_s_at	0.45	1.56	4.5	42 P
M27093_s_at	0.50	1.42	Undef	40 P
M64752_at	0.45	1.07	4.5	38 P
X03490_s_at	0.35	1.38	3.5	38 P
D28235_s_at	0.40	1.37	6.0	37 P
X62429_s_at	0.45	1.66	3.0	38 P
X07235_s_at	0.44	1.44	4.0	35 P
X95632_s_at	0.45	1.86	9.0	35 P
M27436_s_at	0.45	1.65	4.5	32 P
J00219_s_at	0.40	1.18	8.0	31 P
M26665_at	0.50	1.48	3.0	27 P
U09716_s_at	0.35	1.84	3.5	25 P
X01186_s_at	0.35	0.95	7.0	22 P

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TABLE 8

TABLE 8

Accession	Description	Connect. Tite.	Norm. ureth.	Ta. Gr1	TaGr1d	TaGr1d	TaGr1d
AB000102	Human GABA _A receptor alpha-3 subunit.	351	117	167	170	170	180
AB000111	Human mRNA for "olactonodulin", complete cds	194	62	91	37	42	51
AB000115	Human "mRNA", complete cds	163	106	44	20	76	92
AB000220	Human mRNA for "seraphorm" T ₂ , complete cds	195	78	43	190	28	37
AB000231	Human DNA for GPI-anchored molecule, 3aa "protein", complete cds	42	26	37	188	108	108
AB000408	Human mRNA for "Mink1", complete cds	37	70	20	97	235	20
AB000410	Human RGG3 "mRNA", complete cds	20	20	20	20	20	20
AB000416	Human mRNA for "VRK1", complete cds	113	26	67	30	68	20
AB000440	Human mRNA for "VRK2", complete cds	95	85	53	87	30	42
AB000450	Human "mRNA", clone RES4-22B, complete cds	410	203	643	404	658	309
AB000460	Human mRNA for B14 binding "protein", clone RES4-23A, complete cds	88	103	20	79	213	24
AB000462	Human "mRNA", clone RES4-24A, exon 1-2, 3-4	223	173	199	190	294	250
AB000464	Human "mRNA", clone RES4-24C, exon 1-2, 3	20	20	20	20	20	20
AB000466	Human "mRNA", clone RES4-25, partial cds	20	20	20	20	20	20
AB000468	Human mRNA for zinc finger "protein", clone RES4-26, complete cds	134	99	164	133	268	20
AB000481	Human mRNA for TGF-beta superfamily "protein", complete cds	214	286	1029	839	448	249
AB000584	Human mRNA for "BMAL1b", partial cds, clone AB000318 myope-RNA	25	20	20	20	20	20
AB000595	Human sapiens mRNA for "cathartin" T181, partial cds, clone AB000382 myope-RNA	20	20	20	20	20	20
AB000598	Human sapiens mRNA for "cathartin" T182, partial cds, clone AB000382 myope-RNA	66	76	27	65	72	20
AB000599	Human sapiens mRNA for "cathartin" T183, partial cds, clone AB000382 myope-RNA	98	76	30	20	68	20
AB000599	Human sapiens mRNA for "cathartin" T184, partial cds, clone AB000382 myope-RNA	55	24	20	20	20	103
AB000605	Human DNA for "H ₂ treatment", complete cds	20	20	20	20	20	20
AB001106	Human mRNA for "gile maturation factor", complete cds	491	300	954	532	277	289
AB0011325	Human ADP3 gene for aquaporin 3 (water "channel"), partial cds	24	20	20	20	20	20
AB0002314	Human mRNA for KIAA0316 "gene", complete cds, clone AB0002314 myope-RNA	289	131	241	97	133	112
AB0002315	Human mRNA for KIAA0317 "gene", complete cds, clone AB0002315 myope-RNA	251	97	190	111	190	99
AB0002316	Human mRNA for KIAA0320 "gene", partial cds, clone AB0002316 myope-RNA	27	20	20	20	45	20
AB0002332	Human mRNA for KIAA0334 "gene", complete cds, clone AB0002332 myope-RNA	43	172	259	149	171	96
AB0002355	Human mRNA for KIAA0357 "gene", partial cds, clone AB0002355 myope-RNA	50	35	20	20	20	44
AB0002365	Human mRNA for KIAA0368 "gene", partial cds, clone AB0002365 myope-RNA	20	20	21	20	43	52
AB0002390	Human mRNA for KIAA0382 "gene", partial cds, clone AB0002390 myope-RNA	67	20	156	75	20	24
AB0002409	Human mRNA for KIAA0384 "gene", complete cds, clone AB0002409 myope-RNA	302	145	302	289	272	228
AB0002430	Human sapiens mRNA for "SLC", complete cds, clone AB0002430 myope-RNA	37	58	20	20	36	68
AB0002430	Human mRNA for "Clp1", complete cds	2063	4012	2243	2109	1832	2439
AB0002559	Human mRNA for "proteasome subunit P4.0", complete cds	360	209	249	439	592	502
AB0003102	Human mRNA for "proteasome subunit P5", complete cds	114	67	121	141	357	264
AB0003103	Human mRNA for "proteasome subunit P7", complete cds	43	20	49	30	30	20
AB0003177	Human mRNA for "proteasome subunit P7", complete cds	109	97	89	95	149	127
AB0003698	Human mRNA for "Cdk7-related kinase", complete cds	30	20	20	20	20	20
AB0004684	Human mRNA for "PKU-alpha", partial cds, clone AB0004684 myope-RNA	125	99	73	97	190	60
AB0005535	Human sapiens mRNA for "Cdk4", partial cds, clone AB0005535 myope-RNA	222	158	240	209	498	341
AB0005930	Human sapiens mRNA for "equipoint 3", complete cds, clone AB0005930 myope-RNA	20	20	20	20	20	160
AB0005930	Human sapiens mRNA for "equipoint 4", complete cds, clone AB0005930 myope-RNA	137	307	280	121	497	588
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB0007182	Human sapiens mRNA for "palestin-4", complete cds, clone AB0007182 myope-RNA	23	29	22	20	194	48
AB00							

	Expressed RNA in Subcutaneous connective tissue, Normal urothelium and Transitional cell carcinomas	484	99	20	34	302
Human plasma (excretory) mRNA for glutathione peroxidase, complete cds		1245	761	20	23	261
Human cardiac muscle gamma-actin gene; 5' flank and		20	20	20	20	20
Human mRNA for tyrosine carboxyl protein, a component of cat enzyme complex, glycine synthase (EC 2.12.10)		123	20	84	35	20
Human mRNA for hydroxymethylglutaryl-CoA lyase, exon 1		108	438	184	214	20
Human T cell surface antigen CD7 gene		71	107	101	119	94
Human mRNA for proteinase subunit HC3		310	462	251	300	132
Human mRNA for proteinase subunit HC5		188	69	197	179	68
Human mRNA for proteinase subunit HC6		168	211	237	152	234
Human mRNA for proteinase subunit HC9		20	52	28	20	20
Human mRNA for phospholipid pyrophosphatase synthetase (EC 2.7.6.1) subunit I		47	24	32	41	20
Human mRNA for long-chain acyl-CoA synthetase		82	37	20	20	332
Human mRNA for placental alkaline phosphatase		20	95	20	20	20
Human mRNA for protein kinase C delta type		38	20	20	20	20
Human gene for mitochondrial aspartate-CoA ligase		10	20	20	20	20
Human mRNA for GNA-L protein, complete cds		121	248	190	232	176
Human mRNA for 2-oxoglutarate decarboxylase, complete cds		128	68	20	51	170
Human mRNA for major structural protein of myelin, complete cds		20	20	45	20	20
Human mRNA for CRK-II, complete cds		20	20	25	20	20
Human mRNA for smooth muscle myosin heavy chain		171	40	20	61	202
Human mRNA for choline kinase		110	47	20	61	202
Human mRNA for FALP-related receptor (FAR3)		26	20	57	33	123
Human mRNA for HAI4		132	20	20	33	495
Human gene for serotonergic 1B receptor, complete cds		133	20	20	33	40
Human mRNA for interleukin 2 receptor gamma chain		178	200	199	139	811
Human mRNA for MGS1, complete cds		222	70	70	109	106
Human DNA for enhancer A, "receptor," 5' flanking region and		57	20	20	20	20
Human RNA for protein synthesis "phosphatase," complete cds		20	20	20	20	20
Human mRNA for Eup-ZIPAS-JUPR13(Gas-3) of peripheral myelin, complete cds		557	309	78	128	308
Human mRNA for nucleotide pyrophosphatase, complete cds		85	36	20	31	103
Human mRNA for cytochrome P-450 1B1		52	20	20	20	20
Human mRNA for N1 protein lacertini (neuronal protein), complete cds		86	40	20	20	20
Human mRNA for lysosomal "autophagosome," complete cds		20	20	20	20	20
Human mRNA for autolytic inhibitor factor 4 gamma (H4-gamma)		20	20	20	301	244
Homo sapiens mRNA for ST2 protein		20	20	20	58	20
Human mRNA for erythrocyte-specific ADP deaminase, complete cds		37	63	188	92	176
Human mRNA for ATP synthase subunit c encoded by P1 gene		611	505	578	432	1114
Human Z-DNA cyclonucleoside 3'-phosphatease gene, exon 3		218	235	195	170	188
Human gene for endothelial-B receptor (NET-BR)		20	22	70	41	20
Human mRNA for macrophage scavenger receptor type 1		20	21	20	42	46
Human mRNA for brain cholesteryl ester receptor		20	20	20	132	20
Human mRNA for lactoyl glutathione lyase		173	67	188	66	20
Human APX gene encoding APX nuclear, complete cds		185	153	259	249	322
Human mRNA for annexin associated 120 kDa nuclear protein p120, partial cds(carboxy terminal)		2051	6543	5549	5595	2371
Human mRNA for PIG-F (phospholipid transfer protein class F), complete cds		20	20	32	48	20
Human mRNA for protein-protein phosphatase		62	25	47	20	24
Human mRNA for KIAA0002 gene, complete cds		42	20	51	49	70
Human mRNA for KIAA0003 gene, complete cds		155	147	128	152	103
Human mRNA for KIAA0004 gene, complete cds		98	28	57	32	32
Human mRNA for KIAA0005 gene, complete cds		24	62	20	36	20
Human mRNA for KIAA0006 gene, complete cds		91	41	64	54	71
Human mRNA for KIAA0007 gene, complete cds		96	20	33	40	20
Human mRNA for KIAA0008 gene, complete cds		24	20	67	66	20
Human mRNA for KIAA0010 gene, complete cds		25	20	20	20	20
Human mRNA for KIAA0011 gene, complete cds		40	20	20	20	20
Human mRNA for KIAA0012 gene, complete cds		100	70	78	36	20
Human mRNA for KIAA0002 gene, complete cds		131	313	20	118	325
Human mRNA for KIAA0016 gene, complete cds		104	123	300	170	280
Human mRNA for KIAA0017 gene, complete cds		110	20	61	55	156
Human mRNA for KIAA0018 gene, complete cds		110	20	20	20	227
Human mRNA for KIAA0019 gene, complete cds		115	39	20	20	104
Human mRNA for KIAA0020 gene, complete cds		115	20	20	20	121
Homo sapiens mRNA for cathepsin specific factor 2 (OSF-Zen)		20	20	20	90	62

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Expressed RNA in pluripotential connective tissue, Normal endothelium and Translational cell carcinoma

050003	Human mRNA for "TESK1", complete cds	55	28	61	76	230	185
050011	Human mRNA for KIAA0121 gene, complete cds	103	136	219	69	256	187
050012	Human mRNA for KIAA0122 gene, partial cds	70	127	102	102	591	170
050013	Human mRNA for KIAA0123 gene, partial cds	128	140	294	190	20	171
050014	Human mRNA for KIAA0124 gene, partial cds	20	20	20	63	217	29
050015	Human mRNA for KIAA0125 gene, complete cds	71	20	20	20	20	57
050016	Human mRNA for KIAA0126 gene, complete cds	20	20	20	20	20	40
050017	Human mRNA for KIAA0127 gene, complete cds	61	59	20	20	20	40
050018	Human mRNA for KIAA0128 gene, partial cds	20	20	20	20	20	41
050019	Human mRNA for KIAA0129 gene, complete cds	33	20	20	20	20	41
050020	Human mRNA for KIAA0130 gene, complete cds	24	20	20	55	20	41
050021	Human mRNA for KIAA0131 gene, complete cds	48	45	20	20	20	43
050022	Human mRNA for KIAA0132 gene, complete cds	20	20	20	20	20	43
050023	Human mRNA for KIAA0133 gene, complete cds	20	20	20	20	20	71
050024	Human mRNA for KIAA0134 gene, complete cds	20	20	20	20	20	35
050025	Human mRNA for KIAA0135 gene, partial cds	90	38	20	20	20	34
050026	Human mRNA for KIAA0136 gene, partial cds	20	20	20	20	20	35
050027	Human mRNA for KIAA0137 gene, complete cds	20	20	20	20	20	35
050028	Human mRNA for KIAA0138 gene, complete cds	20	20	20	20	20	35
050029	Human mRNA for KIAA0139 gene, complete cds	20	20	20	20	20	35
050030	Human mRNA for KIAA0140 gene, complete cds	20	20	20	20	20	35
050031	Human mRNA for KIAA0141 gene, complete cds	20	20	20	20	20	35
050032	Human mRNA for KIAA0142 gene, complete cds	20	20	20	20	20	35
050033	Human mRNA for KIAA0143 gene, complete cds	20	20	20	20	20	35
050034	Human mRNA for KIAA0144 gene, complete cds	20	20	20	20	20	35
050035	Human mRNA for KIAA0145 gene, complete cds	20	20	20	20	20	35
050036	Human mRNA for KIAA0146 gene, complete cds	20	20	20	20	20	35
050037	Human mRNA for KIAA0147 gene, complete cds	20	20	20	20	20	35
050038	Human mRNA for KIAA0148 gene, complete cds	20	20	20	20	20	35
050039	Human mRNA for KIAA0149 gene, complete cds	20	20	20	20	20	35
050040	Human mRNA for KIAA0150 gene, partial cds	20	20	20	20	20	35
050041	Human mRNA for KIAA0151 gene, complete cds	20	20	20	20	20	35
050042	Human mRNA for KIAA0152 gene, complete cds	20	20	20	20	20	35
050043	Human mRNA for KIAA0153 gene, partial cds	20	20	20	20	20	35
050044	Human mRNA for KIAA0154 gene, complete cds	20	20	20	20	20	35
050045	Human mRNA for KIAA0155 gene, complete cds	20	20	20	20	20	35
050046	Human mRNA for KIAA0156 gene, complete cds	20	20	20	20	20	35
050047	Human mRNA for KIAA0157 gene, complete cds	20	20	20	20	20	35
050048	Human mRNA for KIAA0158 gene, complete cds	20	20	20	20	20	35
050049	Human mRNA for KIAA0159 gene, complete cds	20	20	20	20	20	35
050050	Human mRNA for KIAA0160 gene, partial cds	20	20	20	20	20	35
050051	Human mRNA for KIAA0161 gene, complete cds	20	20	20	20	20	35
050052	Human mRNA for KIAA0162 gene, complete cds	20	20	20	20	20	35
050053	Human mRNA for KIAA0163 gene, complete cds	20	20	20	20	20	35
050054	Human mRNA for KIAA0164 gene, complete cds	20	20	20	20	20	35
050055	Human mRNA for KIAA0165 gene, complete cds	20	20	20	20	20	35
050056	Human mRNA for KIAA0166 gene, complete cds	20	20	20	20	20	35
050057	Human mRNA for KIAA0167 gene, complete cds	20	20	20	20	20	35
050058	Human mRNA for KIAA0168 gene, complete cds	20	20	20	20	20	35
050059	Human mRNA for KIAA0169 gene, complete cds	20	20	20	20	20	35
050060	Human mRNA for KIAA0170 gene, complete cds	20	20	20	20	20	35
050061	Human mRNA for KIAA0171 gene, complete cds	20	20	20	20	20	35
050062	Human mRNA for KIAA0172 gene, complete cds	20	20	20	20	20	35

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expressed RNA in Submucosal connective tissue, Normal unobese and Transformed cell carcinoma	complete cds	4E
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D06550.at	Human mRNA for serine/threonine protein kinase, complete cds	48	23	64	49	40
D06551.at	Human mRNA for huc, complete cds	52	20	20	20	52
D06552.at	Human mRNA for KIAA0201 gene, partial cds	69	63	69	60	69
D06553.at	Human mRNA for KIAA0202 gene, partial cds	25	108	45	43	95
D06554.at	Human mRNA for KIAA0203 gene, complete cds	20	20	20	20	20
D06555.at	Human mRNA for KIAA0204 gene, complete cds	60	39	102	58	20
D06556.at	Human mRNA for KIAA0205 gene, complete cds	27	37	53	47	62
D06557.at	Human mRNA for KIAA0206 gene, partial cds	31	41	20	35	42
D06558.at	Human mRNA for KIAA0207 gene, complete cds	74	91	171	81	85
D06559.at	Human mRNA for KIAA0208 gene, complete cds	128	20	154	20	87
D06560.at	Human mRNA for KIAA0209 gene, partial cds	58	20	200	20	200
D06561.at	Human mRNA for KIAA0210 gene, complete cds	155	20	20	20	361
D06562.at	Human mRNA for KIAA0211 gene, complete cds	188	215	66	149	165
D06563.at	Human mRNA for KIAA0212 gene, complete cds	73	41	62	104	138
D06564.at	Human mRNA for KIAA0213 gene, complete cds	32	20	20	20	20
D06565.at	Human mRNA for KIAA0215 gene, complete cds	77	20	20	20	20
D06566.at	Human mRNA for KIAA0216 gene, complete cds	45	20	20	22	20
D06567.at	Human mRNA for KIAA0217 gene, partial cds	116	138	45	20	144
D06568.at	Human mRNA for KIAA0218 gene, complete cds	519	1977	4011	427	4376
D06569.at	Human mRNA for KIAA0219 gene, partial cds	91	20	20	20	20
D06570.at	Human mRNA for KIAA0220 gene, complete cds	91	78	20	20	20
D06571.at	Human mRNA for KIAA0221 gene, partial cds	124	124	53	62	108
D06572.at	Human mRNA for KIAA0222 gene, complete cds	68	133	55	26	168
D06573.at	Human mRNA for KIAA0223 gene, partial cds	59	114	68	60	139
D06574.at	Human mRNA for KIAA0224 gene, complete cds	20	20	20	20	31
D06575.at	Human mRNA for KIAA0225 gene, partial cds	34	20	38	48	48
D06576.at	Human mRNA for KIAA0226 gene, complete cds	52	77	121	53	187
D06577.at	Human mRNA for KIAA0227 gene, partial cds	88	42	98	32	103
D06578.at	Human mRNA for KIAA0228 gene, partial cds	20	20	20	20	162
D06579.at	Human mRNA for KIAA0230 gene, partial cds	43	98	53	20	38
D06580.at	Human mRNA for KIAA0231 gene, complete cds	191	198	218	178	281
D06581.at	Human (lambda) DNA for immunoglobulin light chain	20	20	20	20	20
D06582.at	Human (lambda) DNA for immunoglobulin light chain	20	20	20	20	20
D06583.at	Human (lambda) DNA for immunoglobulin light chain	23	20	20	20	20
D06584.at	Human (lambda) DNA for immunoglobulin light chain	222	20	369	344	68
D06585.at	C7 segment gene extracted from Human (Homo sapiens) DNA for immunoglobulin light chain	94	270	178	224	31
D06586.at	Human (lambda) DNA for immunoglobulin light chain	157	53	20	20	31
D06587.at	Human mRNA for KIAA0233 gene, complete cds	24	123	20	20	197
D06588.at	Human mRNA for KIAA0234 gene, complete cds	20	20	20	20	202
D06589.at	Human mRNA for KIAA0235 gene, complete cds	26	20	40	79	20
D06590.at	Human mRNA for KIAA0236 gene, partial cds	20	20	54	108	20
D06591.at	Human mRNA for KIAA0239 gene, partial cds	28	59	71	246	204
D06592.at	Human mRNA for KIAA0240 gene, partial cds	28	20	20	20	20
D06593.at	Human mRNA for KIAA0241 gene, partial cds	46	20	58	28	20
D06594.at	Human mRNA for KIAA0242 gene, complete cds	91	66	20	20	94
D06595.at	Human carboxyl-terminus osteocalcin mRNA for "GSS355", complete cds	43	85	20	49	32
D06596.at	Human carboxyl-terminus bone osteocalcin mRNA for "GSS3788", complete cds	20	20	37	53	32
D06597.at	Human mRNA for "GSS3788", complete cds	20	20	02	20	20
D06598.at	Human carboxyl-terminus osteocalcin mRNA for "GSS3788", complete cds	238	121	431	63	20
D06599.at	Human mRNA for "GSS3788", complete cds	600	311	208	254	242
D06600.at	Human mRNA for KIAA0243 gene, complete cds	20	44	20	142	20
D06601.at	Human mRNA for KIAA0244 gene, partial cds	20	20	20	64	20
D06602.at	Human mRNA for KIAA0247 gene, complete cds	77	23	58	77	64
D06603.at	Human mRNA for KIAA0248 gene, partial cds	20	89	20	44	20
D06604.at	Human mRNA for KIAA0249 gene, complete cds	20	20	20	158	44
D06605.at	Human mRNA for KIAA0250 gene, complete cds	151	96	82	102	129
D06606.at	Human mRNA for KIAA0251 gene, complete cds	151	127	134	235	210
D06607.at	Human mRNA for KIAA0252 gene, partial cds	186	24	364	343	421
D06608.at	Human mRNA for KIAA0253 gene, complete cds	52	22	20	20	20
D06609.at	Human mRNA for KIAA0254 gene, complete cds	35	35	20	41	118
D06610.at	Human mRNA for KIAA0255 gene, complete cds	33	33	20	67	40
D06611.at	Human mRNA for KIAA0256 gene, partial cds	20	20	20	20	20
D06612.at	Human mRNA for KIAA0257 gene, complete cds	20	20	20	20	20
D06613.at	Human mRNA for KIAA0245 gene, complete cds	20	20	20	20	20
D06614.at	Human mRNA for KIAA0246 gene, partial cds	20	20	20	20	20
D06615.at	Human mRNA for KIAA0247 gene, complete cds	20	20	20	20	20
D06616.at	Human mRNA for KIAA0248 gene, partial cds	20	20	20	20	20
D06617.at	Human mRNA for KIAA0249 gene, complete cds	20	20	20	20	20
D06618.at	Human mRNA for KIAA0250 gene, complete cds	20	20	20	20	20
D06619.at	Human mRNA for KIAA0251 gene, complete cds	20	20	20	20	20
D06620.at	Human mRNA for KIAA0252 gene, partial cds	20	20	20	20	20
D06621.at	Human mRNA for KIAA0253 gene, complete cds	20	20	20	20	20
D06622.at	Human mRNA for KIAA0254 gene, complete cds	20	20	20	20	20
D06623.at	Human mRNA for KIAA0255 gene, complete cds	20	20	20	20	20
D06624.at	Human mRNA for KIAA0256 gene, partial cds	20	20	20	20	20
D06625.at	Human mRNA for KIAA0257 gene, complete cds	20	20	20	20	20

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[illegible]

[illegible]

Expressed RNA in Subepithelial connective tissue, Normal urothelium and Transformed cell carcinoma

Accession	Gene	Protein	Length	Weight	PI	Inst	Ref	Notes
U00001	HC3921-H14181	Homodimer Protein Cb ₂ Class 1	51	20	20	106	171	
U00002	HC3925-H14195	Surfactant Protein Sp-A2 Oclt	46	20	47	73	76	
U00003	HC3926-H14198	Surfactant Protein Sp-A1 Delta	20	20	20	20	20	
U00004	HC3930-H14200	Surfactant Protein Sp-A2 Delta	20	20	20	20	20	
U00005	HC3934-H14204	G1 Phase-Specific Gene	20	20	20	20	20	
U00006	HC3938-H14206	Interleukin 9 Receptor (Gp-S7)404	20	20	20	20	20	
U00007	HC3942-H14212	Interleukin 9 Receptor (Gp-S7)404	20	20	20	20	20	
U00008	HC3945-H14215	Interleukin 9 Receptor (Gp-S7)404	20	20	20	20	20	
U00009	HC3954-H14224	Phospholipid Transfer Protein	20	20	20	20	20	
U00010	HC3955-H14225	Phospholipid Transfer Protein	20	20	20	20	20	
U00011	HC3956-H14226	Phospholipid Transfer Protein	20	20	20	20	20	
U00012	HC3957-H14227	Phospholipid Transfer Protein	20	20	20	20	20	
U00013	HC3958-H14228	Phospholipid Transfer Protein	20	20	20	20	20	
U00014	HC3959-H14229	Phospholipid Transfer Protein	20	20	20	20	20	
U00015	HC3960-H14230	Phospholipid Transfer Protein	20	20	20	20	20	
U00016	HC3961-H14231	Phospholipid Transfer Protein	20	20	20	20	20	
U00017	HC3962-H14232	Phospholipid Transfer Protein	20	20	20	20	20	
U00018	HC3963-H14233	Phospholipid Transfer Protein	20	20	20	20	20	
U00019	HC3964-H14234	Phospholipid Transfer Protein	20	20	20	20	20	
U00020	HC3965-H14235	Phospholipid Transfer Protein	20	20	20	20	20	
U00021	HC3966-H14236	Phospholipid Transfer Protein	20	20	20	20	20	
U00022	HC3967-H14237	Phospholipid Transfer Protein	20	20	20	20	20	
U00023	HC3968-H14238	Phospholipid Transfer Protein	20	20	20	20	20	
U00024	HC3969-H14239	Phospholipid Transfer Protein	20	20	20	20	20	
U00025	HC3970-H14240	Phospholipid Transfer Protein	20	20	20	20	20	
U00026	HC3971-H14241	Phospholipid Transfer Protein	20	20	20	20	20	
U00027	HC3972-H14242	Phospholipid Transfer Protein	20	20	20	20	20	
U00028	HC3973-H14243	Phospholipid Transfer Protein	20	20	20	20	20	
U00029	HC3974-H14244	Phospholipid Transfer Protein	20	20	20	20	20	
U00030	HC3975-H14245	Phospholipid Transfer Protein	20	20	20	20	20	
U00031	HC3976-H14246	Phospholipid Transfer Protein	20	20	20	20	20	
U00032	HC3977-H14247	Phospholipid Transfer Protein	20	20	20	20	20	
U00033	HC3978-H14248	Phospholipid Transfer Protein	20	20	20	20	20	
U00034	HC3979-H14249	Phospholipid Transfer Protein	20	20	20	20	20	
U00035	HC3980-H14250	Phospholipid Transfer Protein	20	20	20	20	20	
U00036	HC3981-H14251	Phospholipid Transfer Protein	20	20	20	20	20	
U00037	HC3982-H14252	Phospholipid Transfer Protein	20	20	20	20	20	
U00038	HC3983-H14253	Phospholipid Transfer Protein	20	20	20	20	20	
U00039	HC3984-H14254	Phospholipid Transfer Protein	20	20	20	20	20	
U00040	HC3985-H14255	Phospholipid Transfer Protein	20	20	20	20	20	
U00041	HC3986-H14256	Phospholipid Transfer Protein	20	20	20	20	20	
U00042	HC3987-H14257	Phospholipid Transfer Protein	20	20	20	20	20	
U00043								

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Accession	Gene	Protein	Function	Ref
U00001	Human p38 mitogen-activated protein kinase	MAP kinase	MAP kinase	1
U00002	Human C/EBP-1 transcription factor	C/EBP-1	Transcription factor	2
U00003	Human alpha-1 antitrypsin	Alpha-1 antitrypsin	Alpha-1 antitrypsin	3
U00004	Human alpha-2 macroglobulin	Alpha-2 macroglobulin	Alpha-2 macroglobulin	4
U00005	Human alpha-1B globulin	Alpha-1B globulin	Alpha-1B globulin	5
U00006	Human alpha-1A globulin	Alpha-1A globulin	Alpha-1A globulin	6
U00007	Human alpha-1C globulin	Alpha-1C globulin	Alpha-1C globulin	7
U00008	Human alpha-1D globulin	Alpha-1D globulin	Alpha-1D globulin	8
U00009	Human alpha-1E globulin	Alpha-1E globulin	Alpha-1E globulin	9
U00010	Human alpha-1F globulin	Alpha-1F globulin	Alpha-1F globulin	10
U00011	Human alpha-1G globulin	Alpha-1G globulin	Alpha-1G globulin	11
U00012	Human alpha-1H globulin	Alpha-1H globulin	Alpha-1H globulin	12
U00013	Human alpha-1I globulin	Alpha-1I globulin	Alpha-1I globulin	13
U00014	Human alpha-1J globulin	Alpha-1J globulin	Alpha-1J globulin	14
U00015	Human alpha-1K globulin	Alpha-1K globulin	Alpha-1K globulin	15
U00016	Human alpha-1L globulin	Alpha-1L globulin	Alpha-1L globulin	16
U00017	Human alpha-1M globulin	Alpha-1M globulin	Alpha-1M globulin	17
U00018	Human alpha-1N globulin	Alpha-1N globulin	Alpha-1N globulin	18
U00019	Human alpha-1O globulin	Alpha-1O globulin	Alpha-1O globulin	19
U00020	Human alpha-1P globulin	Alpha-1P globulin	Alpha-1P globulin	20
U00021	Human alpha-1Q globulin	Alpha-1Q globulin	Alpha-1Q globulin	21
U00022	Human alpha-1R globulin	Alpha-1R globulin	Alpha-1R globulin	22
U00023	Human alpha-1S globulin	Alpha-1S globulin	Alpha-1S globulin	23
U00024	Human alpha-1T globulin	Alpha-1T globulin	Alpha-1T globulin	24
U00025	Human alpha-1U globulin	Alpha-1U globulin	Alpha-1U globulin	25
U00026	Human alpha-1V globulin	Alpha-1V globulin	Alpha-1V globulin	26
U00027	Human alpha-1W globulin	Alpha-1W globulin	Alpha-1W globulin	27
U00028	Human alpha-1X globulin	Alpha-1X globulin	Alpha-1X globulin	28
U00029	Human alpha-1Y globulin	Alpha-1Y globulin	Alpha-1Y globulin	29
U00030	Human alpha-1Z globulin	Alpha-1Z globulin	Alpha-1Z globulin	30
U00031	Human alpha-1AA globulin	Alpha-1AA globulin	Alpha-1AA globulin	31
U00032	Human alpha-1AB globulin	Alpha-1AB globulin	Alpha-1AB globulin	32
U00033	Human alpha-1AC globulin	Alpha-1AC globulin	Alpha-1AC globulin	33
U00034	Human alpha-1AD globulin	Alpha-1AD globulin	Alpha-1AD globulin	34
U00035	Human alpha-1AE globulin	Alpha-1AE globulin	Alpha-1AE globulin	35
U00036	Human alpha-1AF globulin	Alpha-1AF globulin	Alpha-1AF globulin	36
U00037	Human alpha-1AG globulin	Alpha-1AG globulin	Alpha-1AG globulin	37
U00038	Human alpha-1AH globulin	Alpha-1AH globulin	Alpha-1AH globulin	38
U00039	Human alpha-1AI globulin	Alpha-1AI globulin	Alpha-1AI globulin	39
U00040	Human alpha-1AJ globulin	Alpha-1AJ globulin	Alpha-1AJ globulin	40
U00041	Human alpha-1AK globulin	Alpha-1AK globulin	Alpha-1AK globulin	41
U00042	Human alpha-1AL globulin	Alpha-1AL globulin	Alpha-1AL globulin	42
U00043	Human alpha-1AM globulin	Alpha-1AM globulin	Alpha-1AM globulin	43
U00044	Human alpha-1AN globulin	Alpha-1AN globulin	Alpha-1AN globulin	44
U00045	Human alpha-1AO globulin	Alpha-1AO globulin	Alpha-1AO globulin	45
U00046	Human alpha-1AP globulin	Alpha-1AP globulin	Alpha-1AP globulin	46
U00047	Human alpha-1AQ globulin	Alpha-1AQ globulin	Alpha-1AQ globulin	47
U00048	Human alpha-1AR globulin	Alpha-1AR globulin	Alpha-1AR globulin	48
U00049	Human alpha-1AS globulin	Alpha-1AS globulin	Alpha-1AS globulin	49
U00050	Human alpha-1AT globulin	Alpha-1AT globulin	Alpha-1AT globulin	50
U00051	Human alpha-1AU globulin	Alpha-1AU globulin	Alpha-1AU globulin	51
U00052	Human alpha-1AV globulin	Alpha-1AV globulin	Alpha-1AV globulin	52
U00053	Human alpha-1AW globulin	Alpha-1AW globulin	Alpha-1AW globulin	53
U00054	Human alpha-1AX globulin	Alpha-1AX globulin	Alpha-1AX globulin	54
U00055	Human alpha-1AY globulin	Alpha-1AY globulin	Alpha-1AY globulin	55
U00056	Human alpha-1AZ globulin	Alpha-1AZ globulin	Alpha-1AZ globulin	56
U00057	Human alpha-1BA globulin	Alpha-1BA globulin	Alpha-1BA globulin	57
U00058	Human alpha-1BB globulin	Alpha-1BB globulin	Alpha-1BB globulin	58
U00059	Human alpha-1BC globulin	Alpha-1BC globulin	Alpha-1BC globulin	59
U00060	Human alpha-1BD globulin	Alpha-1BD globulin	Alpha-1BD globulin	60
U00061	Human alpha-1BE globulin	Alpha-1BE globulin	Alpha-1BE globulin	61
U00062	Human alpha-1BF globulin	Alpha-1BF globulin	Alpha-1BF globulin	62
U00063	Human alpha-1BG globulin	Alpha-1BG globulin	Alpha-1BG globulin	63
U00064				

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[illegible]

Accession	Gene	Chromosome	Start	End	Strand	Size (bp)	GC (%)	Exons	Introns	UTR	5'UTR	3'UTR	ORF (aa)	Protein	Function	Ref
M18890	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18891	Human cyclophilin C (cyclophilin C)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Cyclophilin C	1
M18892	Human placental growth factor (PDGFA)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Placental growth factor	1
M18893	Human placental growth factor (PDGFB)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Placental growth factor	1
M18894	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18895	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18896	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18897	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18898	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18899	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18900	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18901	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18902	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18903	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18904	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18905	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18906	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18907	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18908	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18909	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18910	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18911	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18912	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18913	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18914	Human small proline rich protein (SPR)	12p	441	705	+	264	42.1	1	0	1	20	20	99	32	Small proline rich protein	1
M18915	Human small proline rich protein (SPR)															

Gene	Accession	Length	GC	GC3	GC3+4	GC3-4	GC3-5	GC3-6	GC3-7	GC3-8	GC3-9	GC3-10	GC3-11	GC3-12	GC3-13	GC3-14	GC3-15	GC3-16	GC3-17	GC3-18	GC3-19	GC3-20	GC3-21	GC3-22	GC3-23	GC3-24	GC3-25	GC3-26	GC3-27	GC3-28	GC3-29	GC3-30	GC3-31	GC3-32	GC3-33	GC3-34	GC3-35	GC3-36	GC3-37	GC3-38	GC3-39	GC3-40	GC3-41	GC3-42	GC3-43	GC3-44	GC3-45	GC3-46	GC3-47	GC3-48	GC3-49	GC3-50	GC3-51	GC3-52	GC3-53	GC3-54	GC3-55	GC3-56	GC3-57	GC3-58	GC3-59	GC3-60	GC3-61	GC3-62	GC3-63	GC3-64	GC3-65	GC3-66	GC3-67	GC3-68	GC3-69	GC3-70	GC3-71	GC3-72	GC3-73	GC3-74	GC3-75	GC3-76	GC3-77	GC3-78	GC3-79	GC3-80	GC3-81	GC3-82	GC3-83	GC3-84	GC3-85	GC3-86	GC3-87	GC3-88	GC3-89	GC3-90	GC3-91	GC3-92	GC3-93	GC3-94	GC3-95	GC3-96	GC3-97	GC3-98	GC3-99	GC3-100	GC3-101	GC3-102	GC3-103	GC3-104	GC3-105	GC3-106	GC3-107	GC3-108	GC3-109	GC3-110	GC3-111	GC3-112	GC3-113	GC3-114	GC3-115	GC3-116	GC3-117	GC3-118	GC3-119	GC3-120	GC3-121	GC3-122	GC3-123	GC3-124	GC3-125	GC3-126	GC3-127	GC3-128	GC3-129	GC3-130	GC3-131	GC3-132	GC3-133	GC3-134	GC3-135	GC3-136	GC3-137	GC3-138	GC3-139	GC3-140	GC3-141	GC3-142	GC3-143	GC3-144	GC3-145	GC3-146	GC3-147	GC3-148	GC3-149	GC3-150	GC3-151	GC3-152	GC3-153	GC3-154	GC3-155	GC3-156	GC3-157	GC3-158	GC3-159	GC3-160	GC3-161	GC3-162	GC3-163	GC3-164	GC3-165	GC3-166	GC3-167	GC3-168	GC3-169	GC3-170	GC3-171	GC3-172	GC3-173	GC3-174	GC3-175	GC3-176	GC3-177	GC3-178	GC3-179	GC3-180	GC3-181	GC3-182	GC3-183	GC3-184	GC3-185	GC3-186	GC3-187	GC3-188	GC3-189	GC3-190	GC3-191	GC3-192	GC3-193	GC3-194	GC3-195	GC3-196	GC3-197	GC3-198	GC3-199	GC3-200	GC3-201	GC3-202	GC3-203	GC3-204	GC3-205	GC3-206	GC3-207	GC3-208	GC3-209	GC3-210	GC3-211	GC3-212	GC3-213	GC3-214	GC3-215	GC3-216	GC3-217	GC3-218	GC3-219	GC3-220	GC3-221	GC3-222	GC3-223	GC3-224	GC3-225	GC3-226	GC3-227	GC3-228	GC3-229	GC3-230	GC3-231	GC3-232	GC3-233	GC3-234	GC3-235	GC3-236	GC3-237	GC3-238	GC3-239	GC3-240	GC3-241	GC3-242	GC3-243	GC3-244	GC3-245	GC3-246	GC3-247	GC3-248	GC3-249	GC3-250	GC3-251	GC3-252	GC3-253	GC3-254	GC3-255	GC3-256	GC3-257	GC3-258	GC3-259	GC3-260	GC3-261	GC3-262	GC3-263	GC3-264	GC3-265	GC3-266	GC3-267	GC3-268	GC3-269	GC3-270	GC3-271	GC3-272	GC3-273	GC3-274	GC3-275	GC3-276	GC3-277	GC3-278	GC3-279	GC3-280	GC3-281	GC3-282	GC3-283	GC3-284	GC3-285	GC3-286	GC3-287	GC3-288	GC3-289	GC3-290	GC3-291	GC3-292	GC3-293	GC3-294	GC3-295	GC3-296	GC3-297	GC3-298	GC3-299	GC3-300	GC3-301	GC3-302	GC3-303	GC3-304	GC3-305	GC3-306	GC3-307	GC3-308	GC3-309	GC3-310	GC3-311	GC3-312	GC3-313	GC3-314	GC3-315	GC3-316	GC3-317	GC3-318	GC3-319	GC3-320	GC3-321	GC3-322	GC3-323	GC3-324	GC3-325	GC3-326	GC3-327	GC3-328	GC3-329	GC3-330	GC3-331	GC3-332	GC3-333	GC3-334	GC3-335	GC3-336	GC3-337	GC3-338	GC3-339	GC3-340	GC3-341	GC3-342	GC3-343	GC3-344	GC3-345	GC3-346	GC3-347	GC3-348
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	Expressed RNA in Subcutaneous connective tissue, Normal urothelium and Transitional cell carcinoma	67	2005	2481	20	4500	20	3468	20	1906	20	1616
Human placental protein (PPI1) "mRNA", complete cds												
Human homologue of rat insulinoma gene ("ig"), exon 4-lan												
Human MHC class II HLA-DR beta-1 mRNA (DRB2.3), 5' end												
Human muscle glycogen phosphorylase (PYGM) gene												
Human salivary amylase "gene", 5' flank												
Human steroid 11-beta-hydroxylase (CYP11B1) gene												
Human acridin CP-22 "mRNA", complete cds												
Human Fe-superoxide reductase germin-like protein "mRNA", complete cds												
Human vitellin "mRNA", complete cds												
Human cytochrome P450M4 (CYP2A4) "mRNA", complete cds												
Human cytochrome P450IA3 (CYP2A3) "mRNA", complete cds												
Human CAMP-dependent protein kinase type I gamma subunit (PRKAR1A) "mRNA", complete cds												
Human cell adhesion protein (BQMI) "mRNA", complete cds												
Human 33-kDa prointerleukin protein "mRNA", complete cds												
Human tyrosine-kinase "mRNA", 5' end												
Human HLA-B-associated transcript 2 (BAT2) "gene", 5' flank												
Human HLA-B-associated transcript 3 (BAT3) "gene", 5' end												
Human lymphocyte-specific protein 1 (LSP1) "mRNA", complete cds												
Human MHC class II HLA-DR beta-1 (HLA-DRB1) "mRNA", complete cds												
Human (clone T11 [26.133]) alpha-2 type IV collagen (COL4A2) "mRNA", complete cds												
Human 20-kDa cell surface protein (FAF-1) "mRNA", complete cds												
Human (clone lambda 10-2) nonreceptor tyrosine phosphatase 1 (PTEN1) gene												
Human ornithine decarboxylase "gene", complete cds												
Human fetal skeletal muscle troponin C gene												
Human p78 protein "mRNA", complete cds												
Human carbonic dehydratase I (CAI) "mRNA", complete cds												
Human alpha-2-adrenergic receptor (alpha-2 c2) "gene", complete cds												
Human transforming growth factor-beta 1 binding protein "mRNA", complete cds												
Human cathepsin B "mRNA", complete cds												
Human intracellular calcium-binding protein 1 (Ubp-1) "mRNA", complete cds												
Human beta actinin "mRNA", complete cds												
Human testis-specific calyculin-dependent protein kinase catalytic subunit (C-beta isoform) "mRNA", complete cds												
Human testis-specific protein kinase gamma-subunit "mRNA", complete cds												
Human leucocyte-cell adhesion molecule 1 (ICAM-1) "mRNA", complete cds												
Human plasminogen gene												
Human epidermal growth factor receptor (HER3) "mRNA", complete cds												
Human epimerase synthase "mRNA", complete cds												
Human plasmid glycoprotein III (GPIII) gene												
Human transmembrane tyrosine-specific protein kinase (ROS1) "mRNA", complete cds												
Human saplin (clone lambda MSP131 beta-microglobulin (MSP) gene)												
Human beta-galactosidase (GLB1) "mRNA", complete cds												
Human interferon-gamma-inducible leukinein 2,3-deoxyribose 2,3-diphosphate (IDO) "mRNA", complete cds												
Human lamin B1 "mRNA", complete cds												
Human omega light chain protein 14.1 (lg lambda chain related) gene												
Human omega heavy chain protein 14.1 (lg lambda chain related) gene												
Human FKBP50-binding protein (FKBP) "mRNA", complete cds												
Human elongated protein C-gene "mRNA", complete cds												
Human protein tyrosine phosphatase (PTase-alpha) "mRNA", complete cds												
Human protein kinase C-gene "mRNA", complete cds												
Human pregnancy-specific beta-1-glycoprotein mRNA "mRNA", complete cds												
Human MHC class II alpha glycoprotein (HLA-DQA) "mRNA", 5' end												
Human secretory epithelial tumor nuclear origin (NOC1) "gene", complete cds												
Human melanocortin-4-receptor "gene", complete cds</												

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Accession	Gene	Chromosome	Start	End	Strand	Size	GC	GC3	GC4	GC5	GC6	GC7	GC8	GC9	GC10	GC11	GC12	GC13	GC14	GC15	GC16	GC17	GC18	GC19	GC20	GC21	GC22	GC23	GC24	GC25	GC26	GC27	GC28	GC29	GC30	GC31	GC32	GC33	GC34	GC35	GC36	GC37	GC38	GC39	GC40	GC41	GC42	GC43	GC44	GC45	GC46	GC47	GC48	GC49	GC50	GC51	GC52	GC53	GC54	GC55	GC56	GC57	GC58	GC59	GC60	GC61	GC62	GC63	GC64	GC65	GC66	GC67	GC68	GC69	GC70	GC71	GC72	GC73	GC74	GC75	GC76	GC77	GC78	GC79	GC80	GC81	GC82	GC83	GC84	GC85	GC86	GC87	GC88	GC89	GC90	GC91	GC92	GC93	GC94	GC95	GC96	GC97	GC98	GC99	GC100	GC101	GC102	GC103	GC104	GC105	GC106	GC107	GC108	GC109	GC110	GC111	GC112	GC113	GC114	GC115	GC116	GC117	GC118	GC119	GC120	GC121	GC122	GC123	GC124	GC125	GC126	GC127	GC128	GC129	GC130	GC131	GC132	GC133	GC134	GC135	GC136	GC137	GC138	GC139	GC140	GC141	GC142	GC143	GC144	GC145	GC146	GC147	GC148	GC149	GC150	GC151	GC152	GC153	GC154	GC155	GC156	GC157	GC158	GC159	GC160	GC161	GC162	GC163	GC164	GC165	GC166	GC167	GC168	GC169	GC170	GC171	GC172	GC173	GC174	GC175	GC176	GC177	GC178	GC179	GC180	GC181	GC182	GC183	GC184	GC185	GC186	GC187	GC188	GC189	GC190	GC191	GC192	GC193	GC194	GC195	GC196	GC197	GC198	GC199	GC200	GC201	GC202	GC203	GC204	GC205	GC206	GC207	GC208	GC209	GC210	GC211	GC212	GC213	GC214	GC215	GC216	GC217	GC218	GC219	GC220	GC221	GC222	GC223	GC224	GC225	GC226	GC227	GC228	GC229	GC230	GC231	GC232	GC233	GC234	GC235	GC236	GC237	GC238	GC239	GC240	GC241	GC242	GC243	GC244	GC245	GC246	GC247	GC248	GC249	GC250	GC251	GC252	GC253	GC254	GC255	GC256	GC257	GC258	GC259	GC260	GC261	GC262	GC263	GC264	GC265	GC266	GC267	GC268	GC269	GC270	GC271	GC272	GC273	GC274	GC275	GC276	GC277	GC278	GC279	GC280	GC281	GC282	GC283	GC284	GC285	GC286	GC287	GC288	GC289	GC290	GC291	GC292	GC293	GC294	GC295	GC296	GC297	GC298	GC299	GC300	GC301	GC302	GC303	GC304	GC305	GC306	GC307	GC308	GC309	GC310	GC311	GC312	GC313	GC314	GC315	GC316	GC317	GC318	GC319	GC320	GC321	GC322	GC323	GC324	GC325	GC326	GC327	GC328	GC329	GC330	GC331	GC332	GC333	GC334	GC335	GC336	GC337	GC338	GC339	GC340	GC341	GC342	GC343	GC344	GC345	GC346	GC347	GC348	GC349	GC350	GC351	GC352	GC353	GC354	GC355	GC356	GC357	GC358	GC359	GC360	GC361	GC362	GC363	GC364	GC365	GC366	GC367	GC368	GC369	GC370	GC371	GC372	GC373	GC374	GC375	GC376	GC377	GC378	GC379	GC380	GC381	GC382	GC383	GC384	GC385	GC386	GC387	GC388	GC389	GC390	GC391	GC392	GC393	GC394	GC395	GC396	GC397	GC398	GC399	GC400	GC401	GC402	GC403	GC404	GC405	GC406	GC407	GC408	GC409	GC410	GC411	GC412	GC413	GC414	GC415
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Accession	Gene	Chromosome	Start	End	Strand	Size	GC	GC3	GC3+5	GC3-5	GC3-10	GC3-15	GC3-20	GC3-25	GC3-30	GC3-35	GC3-40	GC3-45	GC3-50	GC3-55	GC3-60	GC3-65	GC3-70	GC3-75	GC3-80	GC3-85	GC3-90	GC3-95	GC3-100	GC3-105	GC3-110	GC3-115	GC3-120	GC3-125	GC3-130	GC3-135	GC3-140	GC3-145	GC3-150	GC3-155	GC3-160	GC3-165	GC3-170	GC3-175	GC3-180	GC3-185	GC3-190	GC3-195	GC3-200	GC3-205	GC3-210	GC3-215	GC3-220	GC3-225	GC3-230	GC3-235	GC3-240	GC3-245	GC3-250	GC3-255	GC3-260	GC3-265	GC3-270	GC3-275	GC3-280	GC3-285	GC3-290	GC3-295	GC3-300	GC3-305	GC3-310	GC3-315	GC3-320	GC3-325	GC3-330	GC3-335	GC3-340	GC3-345	GC3-350	GC3-355	GC3-360	GC3-365	GC3-370	GC3-375	GC3-380	GC3-385	GC3-390	GC3-395	GC3-400	GC3-405	GC3-410	GC3-415	GC3-420	GC3-425	GC3-430	GC3-435	GC3-440	GC3-445	GC3-450	GC3-455	GC3-460	GC3-465	GC3-470	GC3-475	GC3-480	GC3-485	GC3-490	GC3-495	GC3-500	GC3-505	GC3-510	GC3-515	GC3-520	GC3-525	GC3-530	GC3-535	GC3-540	GC3-545	GC3-550	GC3-555	GC3-560	GC3-565	GC3-570	GC3-575	GC3-580	GC3-585	GC3-590	GC3-595	GC3-600	GC3-605	GC3-610	GC3-615	GC3-620	GC3-625	GC3-630	GC3-635	GC3-640	GC3-645	GC3-650	GC3-655	GC3-660	GC3-665	GC3-670	GC3-675	GC3-680	GC3-685	GC3-690	GC3-695	GC3-700	GC3-705	GC3-710	GC3-715	GC3-720	GC3-725	GC3-730	GC3-735	GC3-740	GC3-745	GC3-750	GC3-755	GC3-760	GC3-765	GC3-770	GC3-775	GC3-780	GC3-785	GC3-790	GC3-795	GC3-800	GC3-805	GC3-810	GC3-815	GC3-820	GC3-825	GC3-830	GC3-835	GC3-840	GC3-845	GC3-850	GC3-855	GC3-860	GC3-865	GC3-870	GC3-875	GC3-880	GC3-885	GC3-890	GC3-895	GC3-900	GC3-905	GC3-910	GC3-915	GC3-920	GC3-925	GC3-930	GC3-935	GC3-940	GC3-945	GC3-950	GC3-955	GC3-960	GC3-965	GC3-970	GC3-975	GC3-980	GC3-985	GC3-990	GC3-995	GC3-1000	GC3-1005	GC3-1010	GC3-1015	GC3-1020	GC3-1025	GC3-1030	GC3-1035	GC3-1040	GC3-1045	GC3-1050	GC3-1055	GC3-1060	GC3-1065	GC3-1070	GC3-1075	GC3-1080	GC3-1085	GC3-1090	GC3-1095	GC3-1100	GC3-1105	GC3-1110	GC3-1115	GC3-1120	GC3-1125	GC3-1130	GC3-1135	GC3-1140	GC3-1145	GC3-1150	GC3-1155	GC3-1160	GC3-1165	GC3-1170	GC3-1175	GC3-1180	GC3-1185	GC3-1190	GC3-1195	GC3-1200	GC3-1205	GC3-1210	GC3-1215	GC3-1220	GC3-1225	GC3-1230	GC3-1235	GC3-1240	GC3-1245	GC3-1250	GC3-1255	GC3-1260	GC3-1265	GC3-1270	GC3-1275	GC3-1280	GC3-1285	GC3-1290	GC3-1295	GC3-1300	GC3-1305	GC3-1310	GC3-1315	GC3-1320	GC3-1325	GC3-1330	GC3-1335	GC3-1340	GC3-1345	GC3-1350	GC3-1355	GC3-1360	GC3-1365	GC3-1370	GC3-1375	GC3-1380	GC3-1385	GC3-1390	GC3-1395	GC3-1400	GC3-1405	GC3-1410	GC3-1415	GC3-1420	GC3-1425	GC3-1430	GC3-1435	GC3-1440	GC3-1445	GC3-1450	GC3-1455	GC3-1460	GC3-1465	GC3-1470	GC3-1475	GC3-1480	GC3-1485	GC3-1490	GC3-1495	GC3-1500	GC3-1505	GC3-1510	GC3-1515	GC3-1520	GC3-1525	GC3-1530	GC3-1535	GC3-1540	GC3-1545	GC3-1550	GC3-1555	GC3-1560	GC3-1565	GC3-1570	GC3-1575	GC3-1580	GC3-1585	GC3-1590	GC3-1595	GC3-1600	GC3-1605	GC3-1610	GC3-1615	GC3-1620	GC3-1625
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Expressed RNA in Subcutis of connective tissue, Normal urothelial and Transitional cell carcinoma	
Human hawin-containing monocyte/macrophage hem II (HMO2) "miRNA", complete cds	20
Human beta-2-microglobulin (B2M) "miRNA", partial cds	20
Human receptor tyrosine kinase (HER) "miRNA", complete cds	20
Human AUP-ribosyltransferase factor 1 gene	20
Human treacrinembryonic protein (CTD59) gene	20
Human CD19 "miRNA", complete cds	20
Human cathepsin E (CTSE) gene	20
Human adiponectin complement factor D "miRNA", complete cds	20
Human putative opiate receptor "miRNA", complete cds	20
Human v-fos transformation effector protein (fos-1) "miRNA", complete cds	20
Human subunit gamma of the Na ⁺ /K ⁺ ATPase "miRNA", complete cds	20
Human retinoid X receptor beta (RXR-beta) "miRNA", complete cds	20
Human desmoglein 4 "miRNA", complete cds	20
Human desmoglein 3 "miRNA", complete cds	20
Human desmoglein 2 "miRNA", complete cds	20
Human desmoglein 1 "miRNA", complete cds	20
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Expressed RNA in Subcutaneous connective tissue, Normal urothelium and Treated/old cell carcinoma					
S69372_3_at	Cytosolic unlipidated-38 kDa intracellular serine protease inhibitor [human], "placenta", "mRNA", 1465 nt]	129	177	176	185
S69369_3_at	PAX3-transcription factor [human], adult "carcinoma", "mRNA", 1248 nt]	25	98	49	168
S69370_3_at	PAX3-transcription factor (alternatively spliced) [human], adult "carcinoma", "mRNA", 841 nt]	20	20	20	20
S69370_3_at	Bcl-1 tumor suppressor (3' region) [human], breast epithelium, "mRNA", 1485 nt]	20	99	20	49
S69369_3_at	bcl-2 synuclein [human], brain, "mRNA", 730 nt]	33	20	20	25
S69369_3_at	glycogen synthase [human], liver, "mRNA", 2812 nt]	45	45	07	79
S69369_3_at	integrin beta 3 (alternatively spliced), clone beta 3C] [human], erythrocytic cell T-cell, "mRNA", 409 nt]	51	45	64	52
S69369_3_at	thyroid-stimulating hormone alpha subunit [human], Genomic, 307 nt, segment 4 of 4]	20	20	20	20
S69369_3_at	glycine transporter type 1b [human], substantia nigra, "mRNA", 2364 nt]	31	41	20	20
S69369_3_at	cytochrome C [human], kidney, "mRNA", 883 nt]	95	77	44	254
S69369_3_at	ig alpha 2-immunoglobulin A heavy chain subtype 2 (constant) region, germ line] [human], peripheral blood leukocytes, "Genomic", 1179 nt]	1479	3097	812	580
S69369_3_at	acylcholinesterase (AChE domain) [human], tumor cell lines, "Genomic", 847 nt]	20	37	20	314
S69369_3_at	N-CAM-145 kDa neural cell adhesion molecule [human], fetal calf lung cancer cell line "Q52-R", "mRNA", 2860 nt]	107	220	69	311
S69369_3_at	HCCD1P-CDC10 homolog [human], fetal lung, "mRNA", 2314 nt]	124	23	104	127
S69369_3_at	HL-60 acute promyelocytic leukemia cells, "mRNA", 2704 nt]	82	20	175	26
S69369_3_at	GIF-5A cytokine-like protein factor SA (clone cat 9)] [human], placenta, "Genomic", 558 nt]	20	35	20	84
S69369_3_at	GIF-growth inhibitory factor [human], brain, "mRNA", 2015 nt]	20	20	20	20
S69369_3_at	pyruvate carboxylase [human], kidney, "mRNA", 4017 nt]	20	20	20	20
S69369_3_at	cell S to PD-ECGFIP [human], epidermal carcinoma cell line A431, "mRNA", 3' gene, 1718 nt]	301	136	20	646
S69369_3_at	keratin-Melan 16 homology [human], trichothrochial epithelial cells, "mRNA", 976 nt]	1072	58	25	52
S69369_3_at	HPIK1-low molecular weight protein [human], "liposarcoma", "mRNA", 1813 nt]	21	20	172	62
S69369_3_at	HMDUS170-negative cytoskeletal protein [human], thyroid, "mRNA", 3011 nt]	20	59	20	20
S69369_3_at	APR1 antigen-Mab R1 recognized [human], ovarian carcinoma cell line OVCAR-3, "mRNA", 2444 nt]	20	24	60	58
S69369_3_at	insulin like growth factor II (precursor) [human], "Genomic", 1712 nt] (pp-S75149 myp-DNA transfer-mRNA)	346	424	248	418
S69369_3_at	brain-expressed HHCPTX18 homolog [human], HL-60 acute promyelocytic leukemia cells, "mRNA", 2822 nt] (pp-S75205 myp-RNA)	36	20	20	20
S69369_3_at	CD38-Lymphoid cell activation antigen [human], HL-60 acute promyelocytic leukemia cells, "mRNA", 1818 nt]	400	1714	4488	844
S69369_3_at	Type Ia myosin heavy chain (3' region) [human], skeletal muscle, "mRNA", 827 nt]	67	41	20	85
S69369_3_at	AF-4 basic helix-loop helix DNA-binding protein [human], cervical "carcinoma", "mRNA", 2149 nt]	21	20	20	31
S69369_3_at	NF-Y2-NF-E2-like basic leucine zipper transcriptional activator [human], human-induced K562 cells, "mRNA", 2304 nt]	372	186	289	87
S69369_3_at	W-HK factor [human], leukemic cells K562, chronic myeloid leukemia patient, "mRNA", 756 nt]	42	20	46	20
S69369_3_at	cellular reticulate acid binding protein [human], skin, "mRNA", 735 nt]	84	96	20	33
S69369_3_at	ADP-ribosylation factor [human], skeletal muscle, "mRNA", 1354 nt]	93	20	60	20
S69369_3_at	DAX1-1/DSS-AHC critical region on X chromosome, gene 1 [human], adrenal hypoplasia congenita, "cDNA", fetal adrenum gland, mR	20	20	20	20
S69369_3_at	enkephalin-20g b-type protein homolog [human], "tissue", "mRNA", 1009 nt]	54	69	42	35
S69369_3_at	Multimeric poly(epsilon-caprolactone) hydrogel for tissue repair [human], Genomic, 233 nt, segment 13 of 13]	165	231	20	20
S69369_3_at	EZF-4-transcription factor [human], Kidney and testis cells, "mRNA", 1559 nt]	20	222	216	174
S69369_3_at	type IV-A cyclic AMP specific phosphodiesterase HPDE4A [human], 1-cells, "mRNA", 1559 nt]	143	222	216	174
S69369_3_at	HNT-neurotrophin ligand [human], ovarian cancer cell line OC8, "mRNA", 554 nt] (pp-S75236 myp-RNA)	958	1069	219	185
S69369_3_at	nucleoporin intermediate 1-SRP1 homolog [human], cervical carcinoma HeLa cells, "mRNA", 2940 nt]	36	34	81	101
S69369_3_at	MJD1-MJD1 protein (CAG repeat) [human], brain, "mRNA", 1776 nt]	20	81	46	20
S69369_3_at	PAS3-mitochondrial elongation factor homolog [human], "tissue", "mRNA", 1644 nt]	484	596	987	70
S69369_3_at	A-myb-DNA-binding transactivator [human], neuroblastoma BE-215 cells, "mRNA", 1644 nt]	20	20	20	36
S69369_3_at	A-myb-DNA-binding transactivator (3' region) [human], CCRF-CEM T-leukemia line, "mRNA", 831 nt]	20	20	20	20
S69369_3_at	purine aminobutyrate acid transporter type 3 [human], fetal brain, "mRNA", 1991 nt]	20	20	20	20
S69369_3_at	CNG2-cyclic nucleotide-gated cation channel [human], peripheral leukocytes, "Genomic", 784 nt] (pp-S76007 myp-DNA transfer-CC	20	52	20	20
S69369_3_at	b4C [human], brain, "mRNA", 3194 nt]	20	20	20	20
S69369_3_at	NIK-protein tyrosine kinase [human], B lymphocytes, "mRNA", 2608 nt]	30	92	20	36
S69369_3_at	pdxr-fd-tappa B homolog [human], peripheral blood T cells, "mRNA", 3113 nt]	33	20	68	58
S69369_3_at	4R-4AP2-microtubule-associated protein 2.4R [human], brain, "mRNA", 2235 nt]	42	20	20	104
S69369_3_at	corbin-50-catecholamine fluid protein [human], cerebral brain, "mRNA", 2235 nt]	100	20	20	117
S69369_3_at	dopamine D4 receptor (exon 1) [human], brain tumor tissue, "mRNA", 306 nt]	20	42	20	20
S69369_3_at	protein kinase inhibitor [human], neuroblastoma cell line "SH-SY-5Y", "mRNA", 2147 nt]	20	20	20	20
S69369_3_at	prostate-specific membrane antigen (alternatively spliced) [human], primary prostatic tissues, "mRNA", 2752 nt]	65	123	105	52
S69369_3_at	NAV2-NAV oncogene homolog [human], fetal brain, "mRNA", 2752 nt]	20	20	20	20
S69369_3_at	neutrophil receptor alpha subunit1A/C2 alpha subunit [human], thymic "carcinoma", myeloid leukemia-associated thymoma	155	103	20	20
S69369_3_at	TM6SF-NGF-Beta 7 beta-type transduction factor homolog [human], T lymphoid cell line "PEER", "mRNA", 2469 nt]	20	20	20	70
S69369_3_at	transcript ch33 [human], TFE1 RF48, stomach cancer cell line, "mRNA", 216 nt] (pp-S77361 myp-RNA)	20	20	20	40
S69369_3_at	transcript ch133 [human], TFE1 RF48, stomach cancer cell line, "mRNA", 216 nt] (pp-S77361 myp-RNA)	20	20	20	20
S69369_3_at	transcript ch133 [human], TFE1 RF48, stomach cancer cell line, "mRNA", 216 nt] (pp-S77361 myp-RNA)	20	20	20	20
S69369_3_at	Type 1 angiotensin II receptor [human], liver, "mRNA", 2208 nt]	61	68	47	138
S69369_3_at	neurotrophin-4 receptor [human], "Genomic", 1671 nt]	55	36	105	93
S69369_3_at	ERV9 reverse transcriptase homolog [clone R111] [human], multiple "adenoma", brain plaques, "mRNA", 84 nt] (pp-S77578 my	96	97	47	196
S69369_3_at	ERV9 reverse transcriptase homolog [clone R111] [human], multiple "adenoma", brain plaques, "mRNA", 84 nt] (pp-S77578 my	20	20	20	20
S69369_3_at	HERV9 reverse transcriptase homolog [clone R1240] [human], multiple "adenoma", brain plaques, "mRNA", 84 nt] (pp-S77578 my	61	96	90	178
S69369_3_at	HERV9 reverse transcriptase homolog [clone R1240] [human], multiple "adenoma", brain plaques, "mRNA", 84 nt] (pp-S77578 my	20	20	20	256
S69369_3_at	HERV9 reverse transcriptase homolog [clone R1240] [human], multiple "adenoma", brain plaques, "mRNA", 84 nt] (pp-S77578 my	52	20	20	118
S69369_3_at	nuclear factor erythroid 2 isoform 1-like basic leucine zipper protein (alternatively spliced), exon 10] [human], fetal liver, "mRNA", 1678 nt]	106	20	20	84

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Accession	Gene	Chromosome	Start	End	Strand	Size	GC	GC3	GC3+5	GC3-5	GC3-1	GC3-2	GC3-3	GC3-4	GC3-5	GC3-6	GC3-7	GC3-8	GC3-9	GC3-10	GC3-11	GC3-12	GC3-13	GC3-14	GC3-15	GC3-16	GC3-17	GC3-18	GC3-19	GC3-20	GC3-21	GC3-22	GC3-23	GC3-24	GC3-25	GC3-26	GC3-27	GC3-28	GC3-29	GC3-30	GC3-31	GC3-32	GC3-33	GC3-34	GC3-35	GC3-36	GC3-37	GC3-38	GC3-39	GC3-40	GC3-41	GC3-42	GC3-43	GC3-44	GC3-45	GC3-46	GC3-47	GC3-48	GC3-49	GC3-50	GC3-51	GC3-52	GC3-53	GC3-54	GC3-55	GC3-56	GC3-57	GC3-58	GC3-59	GC3-60	GC3-61	GC3-62	GC3-63	GC3-64	GC3-65	GC3-66	GC3-67	GC3-68	GC3-69	GC3-70	GC3-71	GC3-72	GC3-73	GC3-74	GC3-75	GC3-76	GC3-77	GC3-78	GC3-79	GC3-80	GC3-81	GC3-82	GC3-83	GC3-84	GC3-85	GC3-86	GC3-87	GC3-88	GC3-89	GC3-90	GC3-91	GC3-92	GC3-93	GC3-94	GC3-95	GC3-96	GC3-97	GC3-98	GC3-99	GC3-100	GC3-101	GC3-102	GC3-103	GC3-104	GC3-105	GC3-106	GC3-107	GC3-108	GC3-109	GC3-110	GC3-111	GC3-112	GC3-113	GC3-114	GC3-115	GC3-116	GC3-117	GC3-118	GC3-119	GC3-120	GC3-121	GC3-122	GC3-123	GC3-124	GC3-125	GC3-126	GC3-127	GC3-128	GC3-129	GC3-130	GC3-131	GC3-132	GC3-133	GC3-134	GC3-135	GC3-136	GC3-137	GC3-138	GC3-139	GC3-140	GC3-141	GC3-142	GC3-143	GC3-144	GC3-145	GC3-146	GC3-147	GC3-148	GC3-149	GC3-150	GC3-151	GC3-152	GC3-153	GC3-154	GC3-155	GC3-156	GC3-157	GC3-158	GC3-159	GC3-160	GC3-161	GC3-162	GC3-163	GC3-164	GC3-165	GC3-166	GC3-167	GC3-168	GC3-169	GC3-170	GC3-171	GC3-172	GC3-173	GC3-174	GC3-175	GC3-176	GC3-177	GC3-178	GC3-179	GC3-180	GC3-181	GC3-182	GC3-183	GC3-184	GC3-185	GC3-186	GC3-187	GC3-188	GC3-189	GC3-190	GC3-191	GC3-192	GC3-193	GC3-194	GC3-195	GC3-196	GC3-197	GC3-198	GC3-199	GC3-200	GC3-201	GC3-202	GC3-203	GC3-204	GC3-205	GC3-206	GC3-207	GC3-208	GC3-209	GC3-210	GC3-211	GC3-212	GC3-213	GC3-214	GC3-215	GC3-216	GC3-217	GC3-218	GC3-219	GC3-220	GC3-221	GC3-222	GC3-223	GC3-224	GC3-225	GC3-226	GC3-227	GC3-228	GC3-229	GC3-230	GC3-231	GC3-232	GC3-233	GC3-234	GC3-235	GC3-236	GC3-237	GC3-238	GC3-239	GC3-240	GC3-241	GC3-242	GC3-243	GC3-244	GC3-245	GC3-246	GC3-247	GC3-248	GC3-249	GC3-250	GC3-251	GC3-252	GC3-253	GC3-254	GC3-255	GC3-256	GC3-257	GC3-258	GC3-259	GC3-260	GC3-261	GC3-262	GC3-263	GC3-264	GC3-265	GC3-266	GC3-267	GC3-268	GC3-269	GC3-270	GC3-271	GC3-272	GC3-273	GC3-274	GC3-275	GC3-276	GC3-277	GC3-278	GC3-279	GC3-280	GC3-281	GC3-282	GC3-283	GC3-284	GC3-285	GC3-286	GC3-287	GC3-288	GC3-289	GC3-290	GC3-291	GC3-292	GC3-293	GC3-294	GC3-295	GC3-296	GC3-297	GC3-298	GC3-299	GC3-300	GC3-301	GC3-302	GC3-303	GC3-304	GC3-305	GC3-306	GC3-307	GC3-308	GC3-309	GC3-310	GC3-311	GC3-312	GC3-313	GC3-314	GC3-315	GC3-316	GC3-317	GC3-318	GC3-319	GC3-320	GC3-321	GC3-322	GC3-323	GC3-324	GC3-325	GC3-326	GC3-327	GC3-328	GC3-329	GC3-330	GC3-331	GC3-332	GC3-333	GC3-334	GC3-335	GC3-336	GC3-337	GC3-338	GC3-339	GC3-340	GC3-341	GC3-342
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Increased RNA in Bulbourethral connective tissue, Normal urothelium and Transitional cell carcinoma

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Expressed RNA in Subcutaneous connective tissues, Normal urothelium and Transitional cell carcinomas	43	62	60	57	123
H sapiens PRKQ1 mRNA	276	115	129	57	123
H sapiens ERCC mRNA	106	55	120	106	55
H sapiens OXA1H mRNA	123	186	164	130	206
H sapiens mRNA for GTP-binding protein	124	115	459	148	988
H sapiens gene for 6-HT2c receptor	164	160	402	250	542
H sapiens mRNA for mesothelioma gliomatous receptor type 4	3953	3471	4032	3987	2040
H sapiens mRNA for ORF	20	20	20	20	20
H sapiens H sapiens mRNA	62	48	79	63	213
H sapiens mRNA for p53 beta subunit of phosphatidylinositol-3-kinase	939	68	80	1144	352
H sapiens alpha NAC mRNA	81	95	98	44	20
H sapiens PPT108 mRNA	101	32	52	96	54
H sapiens Gd5 gene	101	64	103	59	87
H sapiens nov gene, ap-X80923 mypse-DNA tandem-mRNA	20	33	22	20	20
H sapiens HGV mRNA	20	20	27	21	20
H sapiens mRNA (clone p5) for archin	38	25	20	20	20
H sapiens mRNA for PPH beta subunit protein	20	20	20	20	20
H sapiens mRNA for biophary hydroxase-related protein	38	20	20	20	20
H sapiens mRNA for PRKQ1 protein	20	20	20	20	20
H sapiens mRNA for amphipath	20	20	20	20	20
H sapiens mRNA for EURL1 homonin receptor	54	43	68	104	20
H sapiens mRNA for C11 protein	20	20	20	20	20
H sapiens cleaved light chain 5 gene	20	20	20	20	20
H sapiens cleaved light chain 6 gene	20	20	20	20	20
H sapiens DS-1 mRNA	268	395	628	944	371
H sapiens BAP31 mRNA	20	20	20	20	20
H sapiens mRNA for glucose-dependent neutrophilic polypeptide receptor gene	20	20	20	20	20
H sapiens mRNA for Dentis Oligase candidate gene	20	20	20	20	20
H sapiens IL-4 gene splice variant, ap-X81851 mypse-mRNA	38	24	25	24	24
H sapiens mRNA for for vasopressin activated calcium mobilizing receptor-like protein	20	20	20	20	20
H sapiens mRNA for P0071 protein	20	20	20	20	20
H sapiens mRNA for HEB Tm1 receptor	20	20	20	20	20
H sapiens CENX-594 mRNA, 3' UTR, ap-X81895 mypse-mRNA	20	20	20	20	20
H sapiens mRNA for ZID protein	20	20	20	20	20
H sapiens mRNA for HEB-100	20	20	20	20	20
H sapiens mRNA for HEB-100	20	20	20	20	20
H sapiens HEB-2 mRNA for zinc finger protein	114	81	131	20	20
H sapiens HEB-2 mRNA for zinc finger protein	87	129	131	20	20
H sapiens mRNA for cathepsin O	20	20	20	20	20
H sapiens SUG50 mRNA	20	20	20	20	20
H sapiens mRNA for alpha-contractin	27	36	65	48	34
H sapiens mRNA for beta-contractin (PC3)	20	20	20	20	20
H sapiens mRNA for Glutathione transferase K	20	20	20	20	20
H sapiens mRNA for Tact leukin-like protein 1	20	20	20	20	20
H sapiens "fanc" Apo-1 gene (promoter and exon 1), ap-X82279 mypse-DNA tandem-exon	20	20	20	20	20
H sapiens brain 4 mRNA	20	20	20	20	20
H sapiens mRNA for protein	20	20	20	20	20
H sapiens mRNA for protein	20	20	20	20	20
H sapiens mRNA for protein-2	20	20	20	20	20
H sapiens BPR-403 gene for cyclin-related protein	20	20	20	20	20
H sapiens mRNA for Mos-2	20	20	20	20	20
H sapiens protein mRNA for hair keratin acidic 3-1	20	20	20	20	20
H sapiens mRNA for tyrosine phosphatase	20	20	20	20	20
H sapiens mRNA for E4b antigen	1046	482	931	1282	287
H sapiens mRNA for voltage-activated sodium channel	20	20	20	20	20
H sapiens mRNA for thyroid transcription factor 1	20	20	20	20	20
H sapiens Bta-D-glucose cotransport regulator gene	20	20	20	20	20
H sapiens mRNA for DLG2	20	20	20	20	20
H sapiens Bta mRNA for cytoplasmic tyrosine kinase	20	20	20	20	20
H sapiens mRNA for voltage-gated potassium channel, "channin", beta subunit	20	20	20	20	20
H sapiens mRNA for ATP synthase	20	20	20	20	20
H sapiens mRNA for L-actin	20	20	20	20	20
H sapiens mRNA for phosphatidylinositol 3 kinase gamma	20	20	20	20	20
H sapi					

Transfected cells in subcultured connective tissues, fibroblasts, epithelial cells, and T-lymphocytes

[illegible]

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Expressed RNA in Subepithelial connective tissue, (Normal) endothelial and Transendothelial cell carcinoma									
Accession	Gene	Length (bp)	GC (%)	Exons	Introns	UTR	5'UTR	3'UTR	ORF (aa)
X92000	Hs2000	136	51	1	0	0	0	0	136
X92100	Hs2100	136	51	1	0	0	0	0	136
X92200	Hs2200	136	51	1	0	0	0	0	136
X92300	Hs2300	136	51	1	0	0	0	0	136
X92400	Hs2400	136	51	1	0	0	0	0	136
X92500	Hs2500	136	51	1	0	0	0	0	136
X92600	Hs2600	136	51	1	0	0	0	0	136
X92700	Hs2700	136	51	1	0	0	0	0	136
X92800	Hs2800	136	51	1	0	0	0	0	136
X92900	Hs2900	136	51	1	0	0	0	0	136
X93000	Hs3000	136	51	1	0	0	0	0	136
X93100	Hs3100	136	51	1	0	0	0	0	136
X93200	Hs3200	136	51	1	0	0	0	0	136
X93300	Hs3300	136	51	1	0	0	0	0	136
X93400	Hs3400	136	51	1	0	0	0	0	136
X93500	Hs3500	136	51	1	0	0	0	0	136
X93600	Hs3600	136	51	1	0	0	0	0	136
X93700	Hs3700	136	51	1	0	0	0	0	136
X93800	Hs3800	136	51	1	0	0	0	0	136
X93900	Hs3900	136	51	1	0	0	0	0	136
X94000	Hs4000	136	51	1	0	0	0	0	136
X94100	Hs4100	136	51	1	0	0	0	0	136
X94200	Hs4200	136	51	1	0	0	0	0	136
X94300	Hs4300	136	51	1	0	0	0	0	136
X94400	Hs4400	136	51	1	0	0	0	0	136
X94500	Hs4500	136	51	1	0	0	0	0	136
X94600	Hs4600	136	51	1	0	0	0	0	136
X94700	Hs4700	136	51	1	0	0	0	0	136
X94800	Hs4800	136	51	1	0	0	0	0	136
X94900	Hs4900	136	51	1	0	0	0	0	136
X95000	Hs5000	136	51	1	0	0	0	0	136
X95100	Hs5100	136	51	1	0	0	0	0	136
X95200	Hs5200	136	51	1	0	0	0	0	136
X95300	Hs5300	136	51	1	0	0	0	0	136
X95400	Hs5400	136	51	1	0	0	0	0	136
X95500	Hs5500	136	51	1	0	0	0	0	136
X95600	Hs5600	136	51	1	0	0	0	0	136
X95700	Hs5700	136	51	1	0	0	0	0	136
X95800	Hs5800	136	51	1	0	0	0	0	136
X95900	Hs5900	136	51	1	0	0	0	0	136
X96000	Hs6000	136	51	1	0	0	0	0	136
X96100	Hs6100	136	51	1	0	0	0	0	136
X96200	Hs6200	136	51	1	0	0	0	0	136
X96300	Hs6300	136	51	1	0	0	0	0	136
X96400	Hs6400	136	51	1	0	0	0	0	136
X96500	Hs6500	136	51	1	0	0	0	0	136
X96600	Hs6600	136	51	1	0	0	0	0	136
X96700	Hs6700	136	51	1	0	0	0	0	136
X96800	Hs6800	136	51	1	0	0	0	0	136
X96900	Hs6900	136	51	1	0	0	0	0	136
X97000	Hs7000	136	51	1	0	0	0	0	136
X97100	Hs7100	136	51	1	0	0	0	0	136
X97200	Hs7200	136	51	1	0	0	0	0	136
X97300	Hs7300	136	51	1	0	0	0	0	136
X97400	Hs7400	136	51	1	0	0	0	0	136
X97500	Hs7500	136	51	1	0	0	0	0	136
X97600	Hs7600	136	51	1	0	0	0	0	136
X97700	Hs7700	136	51	1	0	0	0	0	136
X97800	Hs7800	136	51	1	0	0	0	0	136
X97900	Hs7900	136	51	1	0	0	0	0	136
X98000	Hs8000	136	51	1	0	0	0	0	136
X98100	Hs8100	136	51	1	0	0	0	0	136
X98200	Hs8200	136	51	1	0	0	0	0	136
X98300	Hs8300	136	51	1	0	0	0	0	136
X98400	Hs8400	136	51	1	0	0	0	0	136
X98500	Hs8500	136	51	1	0	0	0	0	136
X98600	Hs8600	136	51	1	0	0	0	0	136
X98700	Hs8700	136	51	1	0	0	0	0	136
X98800	Hs8800	136	51	1	0	0	0	0	136
X98900	Hs8900	136	51	1	0	0	0	0	136
X99000	Hs9000	136	51	1	0	0	0	0	136
X99100	Hs9100	136	51	1	0	0	0	0	136
X99200	Hs9200	136	51	1	0	0	0	0	136
X99300	Hs9300	136	51	1	0	0	0	0	136
X99400	Hs9400	136	51	1	0	0	0	0	136
X99500	Hs9500	136	51	1	0	0	0	0	136
X99600	Hs9600	136	51	1	0	0	0	0	136
X99700	Hs9700	136	51	1	0	0	0	0	136
X99800	Hs9800	136	51	1	0	0	0	0	136
X99900	Hs9900	136	51	1	0	0	0	0	136

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Genbank	Gene ID	Gene name	covariance
AB000584_at	AB000584	TGF-beta superfamily protein,	av dif neg
AB002533_at	KPNA4	Qip1, :karyopherin alpha 4	av dif neg
AB002559_at	AB002559	hunc18b2,	av dif neg
AB003102_at	AB003102	26S proteasome subunit p44.5,	av dif neg
AB006782_at	AB006782	galectin-9 isoform,	av dif neg
AC002045_xpt2_s_at	AC002045	Chromosome 16 BAC clone CIT987	av dif neg
AC002073_cds1_at	AC002073	PAC clone DJ515N1 from 22q11.2	av dif neg
AC002115_cds1_at	AC002115	DNA from overlapping chromosom	av dif neg
AC002115_cds4_at	AC002115	DNA from overlapping chromosom	av dif neg
AD000082_cds1_at	CH19HHR23	DNA from chromosome 19p13.2 co	av dif neg
AF000562_at	AF000562	uroplakin II mRNA,	av dif neg
AF001359_f_at	AF001359	DNA mismatch repair protein \	av dif neg
AF009368_at	AF009368	Luman mRNA, :Luman "mRNA," /	av dif neg
AF015913_at	SKB1	SKB1Hs mRNA, :skb1 \S. pombe	av dif neg
D00017_at	HUMLIC	lipocortin II, :annexin II	av dif neg
D00408_s_at	HUMXYPFLA	fetal liver cytochrome P-450	av dif neg
D00596_at	HUMTS1	gene for thymidylate synthase,	av dif neg
D00654_at	HUMACTSG7	gene for enteric smooth muscle	av dif neg
D10523_at	HUM2OGDH	2-oxoglutarate dehydrogenase,	av dif neg
D11086_at	HUMIL2RG	interleukin 2 receptor gamma	av dif neg
D11086_at	HUMIL2RG	interleukin 2 receptor gamma	av dif neg
D11094_at	HUMMSS1	MSS1, :proteasome \prosome,	av dif neg
D11327_s_at	HUMLCPTP	protein-tyrosine phosphatase,	av dif neg
D13118_at	HUMATPSCP1	P1 ATP synthase subunit c, :	av dif neg
D13413_ma1_s_at	HUMTA120	tumor-associated 120 kDa nucl	av dif neg
D13843_at	HUMRSC390	KIAA0018 gene, :KIAA0018 gen	av dif neg
D13705_s_at	HUMOMHY	fatty acids omega-hydroxylase	av dif neg
D13748_at	HUM4AI	eukaryotic initiation factor	av dif neg
D14043_at	HUMMGC24	MGC-24, : "MGC-24," complete	av dif neg
D14530_at	HUMRSPT	homolog of yeast ribosomal pro	av dif neg
D14710_at	HUMIPASAS2	ATP synthase alpha subunit,	av dif neg
D16284_at	HUMDSAEC	mitochondrial 3-oxoacyl-CoA t	av dif neg
D16562_at	HUMATPSGL	ATP synthase gamma-subunit \	av dif neg
D16581_at	HUM8ODGTP	8-oxo-dGTPase, : "8-oxo-dGTP	av dif neg
D17516_at	HUMPACAPR	PACAP receptor, :adenylate c	av dif neg
D17516_at	HUMPACAPR	PACAP receptor, :adenylate c	av dif neg
D17525_at	D17525	precursor of P100 serine prot	av dif neg
D21063_at	HUMORFAAA	KIAA0030 gene,	av dif neg
D21261_at	HUMORFFA	KIAA0120 gene, :transgelin 2	av dif neg
D23660_at	HUMRSP	ribosomal protein, : ribosom	av dif neg
D25218_at	HUMORFN	KIAA0112 gene,	av dif neg
D25218_at	HUMORFN	KIAA0112 gene,	av dif neg
D25248_at	HUMRES44	mRNA, clone:RES4-4.	av dif neg
D25248_at	HUMRES44	mRNA, clone:RES4-4.	av dif neg
D25278_at	HUMORFO	KIAA0036 gene, :KIAA0036 gen	av dif neg
D25303_at	HUMIAS	Integrin alpha subunit,	av dif neg
D26129_at	HUMRNASA	ribonuclease A \RNase A\),	av dif neg
D26528_at	HUMRNA	RNA helicase, :DEAD/H \Asp-	av dif neg
D26535_s_at	HUMDS	gene for dihydrolipoamide succ	av dif neg
D26599_at	HUMPSH2	proteasome subunit HsC7-1, :	av dif neg
D28383_at	HUMASB42	ATP synthase B chain, 5'UTR	av dif neg
D28589_at	HUMKG1E	mRNA \KIAA00167\), partial se	av dif neg
D28915_at	HUMHCAMAP8	gene for hepatitis C-associate	av dif neg
D29012_at	HUMPSY	proteasome subunit Y, : prot	av dif neg

D29841_at	HUMORFA02	KIAA0052 gene,	av dif neg
D29958_at	HUMORFA10	KIAA0116 gene,	av dif neg
D30855_at	HUMELF4AII	eukaryotic initiation factor	av dif neg
D31764_at	HUMORFKG1C	KIAA0084 gene, :KIAA0084 gen	av dif neg
D31764_at	HUMORFKG1C	KIAA0084 gene, :KIAA0084 gen	av dif neg
D31883_at	HUMORFKG1L	KIAA0059 gene, : KIAA0059 "g	av dif neg
D31884_at	HUMORFKG1M	KIAA0083 gene, :KIAA0083 gen	av dif neg
D31884_at	HUMORFKG1M	KIAA0083 gene, :KIAA0083 gen	av dif neg
D31891_at	HUMORFKG1T	KIAA0087 gene, :SET domain,	av dif neg
D32129_f_at	HUMHLAAD	HLA class-I \\\(HLA-A26\\) heavy	av dif neg
D38047_at	HUMPSP31	28S proteasome subunit p31,	av dif neg
D38555_at	HUMORF008	KIAA0079 gene, :Sec24p, S. C	av dif neg
D38583_at	HUMCOLO	calgizzarin, : "calgizzarin,	av dif neg
D42046_at	HUMKIAAJ	KIAA0083 gene, :DNA2 \\\(DNA r	av dif neg
D42046_at	HUMKIAAJ	KIAA0083 gene, :DNA2 \\\(DNA r	av dif neg
D42047_at	HUMKIAAK	KIAA0089 gene, : KIAA0089 "g	av dif neg
D43682_s_at	HUMVLCAD	very-long-chain acyl-CoA dehy	av dif neg
D45370_at	HUMUPST1	apM2 GS2374 \\\(unknown product	av dif neg
D49396_at	HUMAOP1	Apo1_\\(MER5\\(Aop1-Mouse\\)-lik	av dif neg
D49488_at	HUMHTTP	alpha-tocopherol transfer pro	av dif neg
D49728_at	HUMNAK1	NAK1 DNA binding protein,	av dif neg
D49824_s_at	HUMHLABAA	HLA-B null allele mRNA. :HLA-B	av dif neg
D50840_at	D50825S16	DNA for phosphodiesterase 3B,	av dif neg
D63478_at	KIAA0144	KIAA0144 gene, :KIAA0144 gen	av dif neg
D63479_s_at	D63479	KIAA0145 gene,	av dif neg
D63485_at	KIAA0151	KIAA0151 gene, :KIAA0151 gen	av dif neg
D63486_at	KIAA0152	KIAA0152 gene, :KIAA0152 gen	av dif neg
D63851_at	D63851	unc-18 homologue,	av dif neg
D78129_at	HUMHL1115B	squalene epoxidase,	av dif neg
D78275_at	PSMC6	proteasome subunit p42, :pro	av dif neg
D79205_at	D79205	ribosomal protein L39,	av dif neg
D79984_s_at	D79984	KIAA0162 gene,	av dif neg
D79984_s_at	D79984	KIAA0162 gene,	av dif neg
D80002_at	D80002	KIAA0180 gene,	av dif neg
D82345_at	D82345	NB thymosin beta,	av dif neg
D86425_at	D86425	osteonidogen,	av dif neg
D86974_at	D86974	KIAA0220 gene, : " KIAA0220 "	av dif neg
D86985_at	KIAA0232	KIAA0232 gene, :KIAA0232 gen	av dif neg
D87258_at	D87258	serin protease with IGF-blndi	av dif neg
D87735_at	RPL14	ribosomal protein L14, :ribo	av dif neg
D87953_at	D87953	RTP, : "RTP," complete cds	av dif neg
D89052_at	ATP6F	proton-ATPase-like protein,	av dif neg
HG1034-HT1034_f_at	<empty>	<empty>	av dif neg
HG1400-HT1400_s_at	<empty>	<empty>	av dif neg
HG1428-HT1428_s_at	HG1428-HT1428	: ""Globin, "" Beta"	av dif neg
HG1428-HT1428_s_at	HG1428-HT1428	: ""Globin, "" Beta"	av dif neg
HG1515-HT1515_f_at	HG1515-HT1515	:Transcription Factor Btf3b	av dif neg
HG1515-HT1515_f_at	HG1515-HT1515	:Transcription Factor Btf3b	av dif neg
HG1614-HT1614_at	HG1614-HT1614	:Protein Phosphatase "1," Alp	av dif neg
HG1614-HT1614_at	HG1614-HT1614	:Protein Phosphatase "1," Alp	av dif neg
HG1800-HT1823_at	<empty>	<empty>	av dif neg
HG1872-HT1907_at	<empty>	<empty>	av dif neg
HG1872-HT1907_at	<empty>	<empty>	av dif neg
HG1980-HT2023_at	<empty>	<empty>	av dif neg
HG2147-HT2217_r_at	<empty>	<empty>	av dif neg

HG2147-HT2217_r_at	<empty>	<empty>	av dif neg
HG2149-HT2219_at	<empty>	<empty>	av dif neg
HG2167-HT2237_at	<empty>	<empty>	av dif neg
HG2197-HT2267_s_at	HG2197-HT2267	: "Collage," Type "VII,"	av dif neg
HG2238-HT2321_s_at	HG2238-HT2321	: "Nuclear Mitotic Apparatus P	av dif neg
HG2239-HT2324_r_at	<empty>	<empty>	av dif neg
HG2239-HT2324_r_at	<empty>	<empty>	av dif neg
HG2264-HT2380_at	<empty>	<empty>	av dif neg
HG2279-HT2375_at	HG2279-HT2375	: Triosephosphate Isomerase	av dif neg
HG2566-HT4867_at	HG2566-HT4867	: Microtubule-Associated Prote	av dif neg
HG2788-HT2898_at	HG2788-HT2898	: Calcyclin	av dif neg
HG2815-HT2931_at	<empty>	<empty>	av dif neg
HG2815-HT2931_s_at	<empty>	<empty>	av dif neg
HG2815-HT4023_s_at	<empty>	<empty>	av dif neg
HG2873-HT3017_at	<empty>	<empty>	av dif neg
HG2917-HT3061_f_at	HG2917-HT3061	: "Major Histocompatibility "	av dif neg
HG2917-HT3061_f_at	HG2917-HT3061	: "Major Histocompatibility "	av dif neg
HG2981-HT3127_s_at	<empty>	<empty>	av dif neg
HG2994-HT4850_s_at	<empty>	<empty>	av dif neg
HG3039-HT3200_at	<empty>	<empty>	av dif neg
HG3076-HT3238_s_at	HG3076-HT3238	: "Heterogeneous Nuclear Ribon	av dif neg
HG3107-HT3283_s_at	<empty>	<empty>	av dif neg
HG3107-HT3283_s_at	<empty>	<empty>	av dif neg
HG3111-HT311_at	<empty>	<empty>	av dif neg
HG3214-HT3391_at	<empty>	<empty>	av dif neg
HG3236-HT3413_f_at	<empty>	<empty>	av dif neg
HG3254-HT3431_at	<empty>	<empty>	av dif neg
HG3342-HT3519_s_at	HG3342-HT3519	: Id1	av dif neg
HG3384-HT3541_at	HG3384-HT3541	: Ribosomal Protein L37	av dif neg
HG33-HT33_at	HG33-HT33	<empty>	av dif neg
HG3484-HT3678_s_at	<empty>	<empty>	av dif neg
HG3514-HT3708_at	HG3514-HT3708	: Tropomyosin "Tm30nm," Cytosk	av dif neg
HG3543-HT3739_at	HG3543-HT3739	: Insulin-Like Growth Factor 2	av dif neg
HG3543-HT3739_at	HG3543-HT3739	: Insulin-Like Growth Factor 2	av dif neg
HG3549-HT3751_at	HG3549-HT3751	: Wilms' Tumor-Related Protein	av dif neg
HG3570-HT3773_at	HG3570-HT3773	: Protein Phosphatase Inhibito	av dif neg
HG3576-HT3779_f_at	<empty>	<empty>	av dif neg
HG3576-HT3779_f_at	<empty>	<empty>	av dif neg
HG3731-HT4001_at	<empty>	<empty>	av dif neg
HG384-HT384_at	HG384-HT384	: Ribosomal Protein L26	av dif neg
HG384-HT384_at	HG384-HT384	: Ribosomal Protein L26	av dif neg
HG3945-HT4215_at	<empty>	<empty>	av dif neg
HG3991-HT4261_r_at	<empty>	<empty>	av dif neg
HG4020-HT4290_s_at	HG4020-HT4290	: Transglutaminase	av dif neg
HG4258-HT4528_at	<empty>	<empty>	av dif neg
HG4319-HT4589_at	HG4319-HT4589	: Ribosomal Protein L5	av dif neg
HG4338-HT4808_at	<empty>	<empty>	av dif neg
HG4533-HT4938_at	<empty>	<empty>	av dif neg
HG4542-HT4947_at	HG4542-HT4947	: Ribosomal Protein L10	av dif neg
HG4557-HT4962_r_at	<empty>	<empty>	av dif neg
HG4668-HT5083_s_at	<empty>	<empty>	av dif neg
HG4668-HT5083_s_at	<empty>	<empty>	av dif neg
HG4749-HT5197_at	<empty>	<empty>	av dif neg
HG613-HT613_at	HG613-HT613	: Ribosomal Protein S12	av dif neg
HG613-HT613_at	HG613-HT613	: Ribosomal Protein S12	av dif neg

HG821-HT821_at	<empty>	<empty>	av dif neg
HG880-HT880_at	<empty>	<empty>	av dif neg
HG880-HT880_at	<empty>	<empty>	av dif neg
HG987-HT987_at	HG987-HT987	:Mac25 :Mac25	av dif neg
J00105_s_at	HSMGLO	messenger RNA fragment for the	av dif neg
J02811_at	HUMAPOD	apolipoprotein D mRNA, :apoli	av dif neg
J02811_at	HUMAPOD	apolipoprotein D mRNA, :apoli	av dif neg
J02683_s_at	HUMATPC	ADP/ATP carrier protein mRNA,	av dif neg
J02783_at	HUMTHBP	thyroid hormone binding protei	av dif neg
J02874_at	HUMALBP	adipocyte lipid-binding protei	av dif neg
J02874_at	HUMALBP	adipocyte lipid-binding protei	av dif neg
J02902_at	HUMP2A	protein phosphatase 2A regulat	av dif neg
J02908_at	HUMCYPIIF	cytochrome P450IIF1 protein \	av dif neg
J03077_s_at	HUMGLBA	co-beta glucosidase \proactiv	av dif neg
J03242_s_at	HUMGFIL2	insulin-like growth factor II m	av dif neg
J03242_s_at	HUMGFIL2	insulin-like growth factor II m	av dif neg
J03592_at	HUMTLCA	ADP/ATP translocase mRNA, 3' e	av dif neg
J03758_at	HUMGHVA	growth hormone-variant \GH1\)	av dif neg
J03801_f_at	HUMLSZ	lysozyme mRNA, complete cds wi	av dif neg
J03909_at	HUMIIP	gamma-interferon-inducible pro	av dif neg
J03909_at	HUMIIP	gamma-interferon-inducible pro	av dif neg
J03934_s_at	HUMNMOR	Human, NAD(P)H:menadione oxi	av dif neg
J04093_s_at	HUMUGT1FA	phenol UDP-glucuronosyltransfe	av dif neg
J04093_s_at	HUMUGT1FA	phenol UDP-glucuronosyltransfe	av dif neg
J04152_ma1_s_at	HUMGA733A	gastrointestinal tumor-associa	av dif neg
J04164_at	HUM927A	interferon-inducible protein 9	av dif neg
J04164_at	HUM927A	interferon-inducible protein 9	av dif neg
J04173_at	HUMPGAM	phosphoglycerate mutase \PGAM	av dif neg
J04611_at	HUMANP70	lupus p70 \Ku\ autoantigen p	av dif neg
J04615_at	HUMSNRAA	lupus autoantigen \small nucl	av dif neg
J04617_s_at	HUMEF1A	elongation factor EF-1-alpha g	av dif neg
J04873_at	HUMCOR2M	cytochrome bc-1 complex core p	av dif neg
J05036_s_at	HUMCTSE	cathepsin E mRNA, :cathepsin	av dif neg
J05036_s_at	HUMCTSE	cathepsin E mRNA, :cathepsin	av dif neg
J05272_at	HUMIMPH	IMP dehydrogenase type 1 mRNA	av dif neg
K02405_f_at	HUMMHDC3B	MHC class II HLA-DC-3-beta gen	av dif neg
K03189_f_at	HUMCGBEL03	chorionic gonadotropin beta su	av dif pos
K03430_at	HUMC1QB2	complement C1q B-chain gene, e	av dif pos
K03430_at	HUMC1QB2	complement C1q B-chain gene, e	av dif pos
L00634_s_at	HUMFPTA	farnesyl-protein transferase a	av dif pos
L02328_f_at	HUMPREBLYM	\clone Hu lambda-17\ lambda-	av dif pos
L04270_at	HUMTNFRRP	\clone CD18\ tumor necrosis	av dif pos
L04483_s_at	HUMRPS21X	ribosomal protein S21 \RPS21	av dif pos
L04490_at	HUMNADH	\clone CC6\ NADH-ubiquinone	av dif pos
L05072_s_at	HUMIFNRF1A	interferon regulatory factor 1	av dif pos
L05188_f_at	HUMSPRR2B	small proline-rich protein 2	av dif pos
L06499_at	HUMRPL37A	ribosomal protein L37a \RPL37	av dif pos
L06505_at	HUML12A	ribosomal protein L12 mRNA, :	av dif pos
L06797_s_at	HUMGPCR	\clone L5\ orphan G protein-	av dif pos
L06797_s_at	HUMGPCR	\clone L5\ orphan G protein-	av dif pos
L07044_at	HUMCCDPKB	calcium/calmodulin-dependent p	av dif pos
L08666_at	HUMPORIN	porin \por\ mRNA, complete c	av dif pos
L09209_s_at	HUMAMYLOID	amyloid protein homologue mRNA	av dif pos
L10413_at	HUMFTA	farnesyltransferase alpha-subu	av dif pos
L11566_at	HUMRPL18A	ribosomal protein L18 \RPL18	av dif pos

L11672_at	HUMKRUPZN	Kruppel related zinc finger pr	av dif pos
L11708_at	HUMB17HSD	17 beta hydroxysteroid dehydro	av dif pos
L11708_at	HUMB17HSD	17 beta hydroxysteroid dehydro	av dif pos
L12711_s_at	HUMTRANSKE	transketolase \(\text{tk}\) mRNA, :"	av dif pos
L12711_s_at	HUMTRANSKE	transketolase \(\text{tk}\) mRNA, :"	av dif pos
L19493_s_at	HUMFMR1R	FMR1 gene, 3'end.	av dif pos
L19527_at	HUMRPL27	ribosomal protein L27 \(\text{RPL27}\)	av dif pos
L19686_ma1_at	HUMMIF	macrophage migration inhibitor	av dif pos
L19686_ma1_at	HUMMIF	macrophage migration inhibitor	av dif pos
L19779_at	HUMH2A2A	histone H2A.2 mRNA, :H2A hist	av dif pos
L20688_at	HUMLYGDI	GDP-dissociation inhibitor pro	av dif pos
L20941_at	HUMFERRITH	ferritin heavy chain mRNA, :f	av dif pos
L21954_at	HSPBR4	peripheral benzodiazepine rece	av dif pos
L21954_at	HSPBR4	peripheral benzodiazepine rece	av dif pos
L26247_at	HUMSUIISO	sui1 iso1 mRNA,	av dif pos
L27943_at	HUMCYDE	cytidine deaminase \(\text{CDA}\) mRN	av dif pos
L32866_at	HUMEPR1NP	effector cell protease recepto	av dif pos
L32976_at	HUMMLK3A	protein kinase \(\text{MLK-3}\) mRNA,	av dif pos
L33075_at	HUMIQGA	ras GTPase-activating-like pro	av dif pos
L33243_at	HUMPKD1A	polycystic kidney disease 1 pr	av dif pos
L33842_ma1_at	HUMIMPDH	\(\text{clone FFE-7}\) type II inosin	av dif pos
L33842_ma1_at	HUMIMPDH	\(\text{clone FFE-7}\) type II inosin	av dif pos
L33930_s_at	HUMCD24B	CD24 signal transducer mRNA, c	av dif pos
L37127_at	HUMRPIA	RNA polymerase II mRNA, :poly	av dif pos
L38490_s_at	HUMADPRF	ADP-ribosylation factor mRNA,	av dif pos
L38928_at	HUMMETSYN	5,10-methenyltetrahydrofolate	av dif pos
L38941_at	HUMRPL34A	ribosomal protein L34 \(\text{RPL34}\)	av dif pos
L39059_at	HUMTFSL1A	transcription factor SL1 mRNA,	av dif pos
L40357_at	HUMTRIP7M	thyroid receptor interactor \(\text{}	av dif pos
L40379_at	HUMTRIP10M	thyroid receptor interactor \(\text{}	av dif pos
L40387_at	HUMTRIP14G	thyroid receptor interactor \(\text{}	av dif pos
L40392_at	HUMORFB	\(\text{clone S164}\) mRNA, 3' end of	av dif pos
L40904_at	HUMPPARGB	H. sapiens peroxisome prolifer	av dif pos
L41870_at	HUMRB1MRNA	retinoblastoma susceptibility	av dif pos
L42176_at	HUMDRAL	\(\text{clone 35.3}\) DRAL mRNA, :(\	av dif pos
L42373_at	HUMPP2A	phosphatase 2A B56-alpha \(\text{PP2}	av dif pos
L42542_at	HUMRIP1R	RLIP76 protein mRNA, :RLIP76	av dif pos
L76159_at	HUMFRG1R	FRG1 mRNA, :FSHD region gene	av dif pos
L76465_at	HUMPGDHB	NAD+-dependent 15 hydroxyprost	av dif pos
L77888_at	HUMPTPC	protein tyrosine phosphatase m	av dif pos
M10612_at	HUMAPOCII	apolipoprotein C-II gene,	av dif pos
M11119_at	HUMERRNA	endogenous retrovirus envelope	av dif pos
M11147_at	HUMFERL	ferritin L chain mRNA, :ferri	av dif pos
M11313_s_at	HUMA2M	alpha-2-macroglobulin mRNA, :	av dif pos
M11353_at	HUMHISH3C	H3.3 histone class C mRNA,	av dif pos
M12529_at	HUMAPOE	apolipoprotein E mRNA, :apoli	av dif pos
M12529_at	HUMAPOE	apolipoprotein E mRNA, :apoli	av dif pos
M12888_at	HUMTCBY	T-cell receptor active beta-ch	av dif pos
M12888_at	HUMTCBY	T-cell receptor active beta-ch	av dif pos
M13207_at	HUMCSFGMA	granulocyte-macrophage colony-	av dif pos
M13580_s_at	HUMIAIG8	la-associated invariant gamma-	av dif pos
M13666_at	HUMCMYBB	c-myb mRNA, 3' end.	av dif pos
M13755_at	HUMIFN15K	interferon-induced 17-kDa/15-k	av dif pos
M13829_s_at	HUMPKS	putative raf related protein	av dif pos
M13829_s_at	HUMPKS	putative raf related protein	av dif pos

M13903_at	HUMINV2	involucrin gene, exon 2. :invo	av dif pos
M13929_s_at	HUMMYCPOA	c-myc-P64 mRNA, initiating fro	av dif pos
M13929_s_at	HUMMYCPOA	c-myc-P64 mRNA, initiating fro	av dif pos
M13934_cds2_at	HUMRPS14	ribosomal protein S14 gene, :	av dif pos
M13955_at	HUMKERMII	mesothelial keratin K7 \type	av dif pos
M14199_s_at	HUMLAMR	laminin receptor \2H5 epitope	av dif pos
M14199_s_at	HUMLAMR	laminin receptor \2H5 epitope	av dif pos
M14328_s_at	HUMENOA	alpha enolase mRNA, :enolase	av dif pos
M14483_ma1_s_at	HUMTHYMAA	prothymosin alpha mRNA,	av dif pos
M14876_at	HUMSLK	src-like kinase \sik\ mRNA,	av dif pos
M14876_at	HUMSLK	src-like kinase \sik\ mRNA,	av dif pos
M15395_at	HUMLAP	leukocyte adhesion protein \L	av dif pos
M15661_at	HUMRPZH21	ribosomal protein mRNA, :ribo	av dif pos
M15661_at	HUMRPZH21	ribosomal protein mRNA, :ribo	av dif pos
M16038_at	HUMLYN	lyn mRNA encoding a tyrosine k	av dif pos
M17733_at	HUMTHYB4	thymosin beta-4 mRNA, :thymos	av dif pos
M17883_s_at	HUMFFI2B	preproinsulin-like growth fact	av dif pos
M17883_s_at	HUMFFI2B	preproinsulin-like growth fact	av dif pos
M17885_at	HUMPPARP0	acidic ribosomal phosphoprotei	av dif pos
M17886_at	HUMPPARP1	acidic ribosomal phosphoprotei	av dif pos
M18000_at	HUMRPS17A	ribosomal protein S17 gene, :	av dif pos
M18737_ma1_at	HUMHFSP	Hanukah factor serine protease	av dif pos
M19045_f_at	HUMLSZH	lysozyme mRNA, :lysozyme ""m	av dif pos
M19159_at	HUMALPPD	placental heat-stable alkaline	av dif pos
M19159_at	HUMALPPD	placental heat-stable alkaline	av dif pos
M19301_at	HUMKAD	branched-chain alpha-keto acid	av dif pos
M19878_s_at	HUMCALB01	calbindin 27 gene, exons 1 and	av dif pos
M20902_at	HUMAPOCIA	apolipoprotein C-I \VLDL\ ge	av dif pos
M20902_at	HUMAPOCIA	apolipoprotein C-I \VLDL\ ge	av dif pos
M21142_cds2_s_at	HUMGNAS6	guanine nucleotide-binding pro	av dif pos
M21142_cds2_s_at	HUMGNAS6	guanine nucleotide-binding pro	av dif pos
M21186_at	HUMNCBLCA	neutrophil cytochrome b light	av dif pos
M21186_at	HUMNCBLCA	neutrophil cytochrome b light	av dif pos
M21302_at	HUMSPR2B	small proline rich protein \s	av dif pos
M21984_at	HUMTRT	\clone PWHTnT16\ skeletal mu	av dif pos
M22490_at	HUMBMP2B	bone morphogenetic protein-2B	av dif pos
M22960_at	HUMPPR	protective protein mRNA, :pro	av dif pos
M23178_s_at	HUMG0S19A	homologue-1 of gene encoding a	av dif pos
M23613_at	HUMNPM	nucleophosmin mRNA, :nucleoph	av dif pos
M24194_at	HUMMHBA123	MHC protein homologous to chic	av dif pos
M24194_at	HUMMHBA123	MHC protein homologous to chic	av dif pos
M24485_s_at	HUMGSTP1G	\clone pHGST-pi\ glutathione	av dif pos
M24486_s_at	HUMPYHBASA	prolyl 4-hydroxylase alpha sub	av dif pos
M25079_s_at	HUMBETGLA	sickle cell beta-globin mRNA,	av dif pos
M25079_s_at	HUMBETGLA	sickle cell beta-globin mRNA,	av dif pos
M25280_at	HUMLNHR	lymph node homing receptor mRN	av dif pos
M26311_s_at	HUMCFA	cystic fibrosis antigen mRNA,	av dif pos
M26311_s_at	HUMCFA	cystic fibrosis antigen mRNA,	av dif pos
M26665_s_at	HUMHIS2X	histatin 2 \HIS2\ mRNA, :hl	av dif pos
M26708_s_at	HUMPTAA	prothymosin alpha mRNA \ProT-	av dif pos
M26730_s_at	HUMQBPC6	mitochondrial ubiquinone-bindl	av dif pos
M27281_at	HUMVPPF	vascular permeability factor m	av dif pos
M27749_r_at	HUMIGLR141	immunoglobulin-related 14.1 pr	av dif pos
M27749_r_at	HUMIGLR141	immunoglobulin-related 14.1 pr	av dif pos
M27826_at	HUMRTVLH3	endogenous retroviral protease	av dif pos

M27891_at	HUMCYS3A3	cystatin C (CST3) gene, exon	av dif pos
M28212_at	HUMRAB6A	GTP-binding protein (RAB6) m	av dif pos
M28882_s_at	HUMMUC18B	MUC18 glycoprotein mRNA, :mel	av dif pos
M28882_s_at	HUMMUC18B	MUC18 glycoprotein mRNA, :mel	av dif pos
M29335_at	HUMMHDOA	MHC class II DO-alpha mRNA,	av dif pos
M29335_at	HUMMHDOA	MHC class II DO-alpha mRNA,	av dif pos
M29610_s_at	HUMGLYE	glycophorin E mRNA, :glycopho	av dif pos
M30818_at	HUMMXB	interferon-induced cellular re	av dif pos
M30938_at	HUMKUP	Ku (p70/p80) subunit mRNA,	av dif pos
M31303_ma1_at	HUMOP18A	oncoprotein 18 (Op18) gene,	av dif pos
M31303_ma1_at	HUMOP18A	oncoprotein 18 (Op18) gene,	av dif pos
M31520_at	HUMRPS24A	ribosomal protein S24 mRNA,	av dif pos
M31520_ma1_s_at	HUMRPS24A	ribosomal protein S24 mRNA, :r	av dif pos
M31627_at	HUMHXPB1	X box binding protein-1 (XBP-	av dif pos
M31994_at	HUMALDC13	aldehyde dehydrogenase (ALDH1	av dif pos
M32053_at	HUMH19	H19 RNA gene,	av dif pos
M32304_s_at	HUMMET	metalloproteinase inhibitor mR	av dif pos
M32405_at	HUMRIGA	homologue of rat insulinoma ge	av dif pos
M32886_at	HUMSRICPA	sorcin CP-22 mRNA, :sorcin :s	av dif pos
M33600_f_at	HUMMHDR1C	MHC class II HLA-DR-beta-1 (H	av dif pos
M33680_at	HUMTAPA1	28-kDa cell surface protein TA	av dif pos
M33684_s_at	HUMPPP1A5	(clone lambda-16-1) non-rece	av dif pos
M34041_at	HUMADRA2RA	alpha-2-adrenergic receptor (av dif pos
M34182_at	HUMPRKACG	testis-specific protein kinase	av dif pos
M34516_at	HUMIGL122	omega light chain protein 14.1	av dif pos
M34516_r_at	HUMIGL122	omega light chain protein 14.1	av dif pos
M34516_r_at	HUMIGL122	omega light chain protein 14.1	av dif pos
M34715_at	HUMPSBGAA	pregnancy-specific beta-1-glyc	av dif pos
M34996_s_at	HUMDQA1A	MHC cell surface glycoprotein	av dif pos
M34996_s_at	HUMDQA1A	MHC cell surface glycoprotein	av dif pos
M35198_at	HUMINTB6A	integrin B-6 mRNA, :integrin,	av dif pos
M35252_at	HUMCOOTAA	CO-029, :transmembrane 4 super	av dif pos
M35878_at	HUMIBP3	insulin-like growth factor-bin	av dif pos
M36072_at	HUMRPL7A	ribosomal protein L7a (surf 3	av dif pos
M37238_s_at	HUMPLC	phospholipase C mRNA, :phosph	av dif pos
M37245_at	HUMIGCTL3	Ig superfamily cytotoxic T-lym	av dif pos
M37245_at	HUMIGCTL3	Ig superfamily cytotoxic T-lym	av dif pos
M37435_at	HUMCSDF1	macrophage-specific colony-sti	av dif pos
M37583_at	HUMHIS2AZ	histone (H2A.Z) mRNA, :hist	av dif pos
M37815_cds1_at	HUMCD284	T-cell membrane glycoprotein C	av dif pos
M38449_s_at	HUMTGFB	transforming growth factor-bet	av dif pos
M38690_at	HUMANTCD9	CD9 antigen mRNA, :CD9 antige	av dif pos
M38690_at	HUMANTCD9	CD9 antigen mRNA, :CD9 antige	av dif pos
M54995_at	HUMCTAP3	connective tissue activation p	av dif pos
M55409_s_at	HUMPANCAN	pancreatic tumor-related prote	av dif pos
M55409_s_at	HUMPANCAN	pancreatic tumor-related prote	av dif pos
M57293_at	HUMPTHSPA	parathyroid hormone-related pe	av dif pos
M57399_at	HUMHBNF1	nerve growth factor (HBNF-1)	av dif pos
M57399_at	HUMHBNF1	nerve growth factor (HBNF-1)	av dif pos
M57466_s_at	HUMMHDP	MHC class II HLA-DP light chai	av dif pos
M57466_s_at	HUMMHDP	MHC class II HLA-DP light chai	av dif pos
M57710_at	HUMBPIGE	IgE-binding protein (epsilon-	av dif pos
M58378_cds1_at	HUMSYN1E13	synapsin I (SYN1) gene, exon	av dif pos
M58525_s_at	HUMCOMTC	catechol-O-methyltransferase	av dif pos
M58525_s_at	HUMCOMTC	catechol-O-methyltransferase	av dif pos

M59216_s_at	UMGABRB1S5	gamma-aminobutyric acid-A (GA	av dif pos
M59371_at	HUMECK	protein tyrosine kinase mRNA,	av dif pos
M59807_at	HUMNK4	NK4 mRNA, :natural killer cel	av dif pos
M59830_at	HUMMHSP2	MHC class III HSP70-2 gene (H	av dif pos
M59911_at	HUMINTA3A	Integrin alpha-3 chain mRNA,	av dif pos
M60483_ma1_s_at	HUMPP2AA	protein phosphatase 2A catalyt	av dif pos
M60854_at	HUMSRAA	ribosomal protein S16 mRNA, :	av dif pos
M61916_at	HUMLAM101	laminin B1 chain mRNA, :lamin	av dif pos
M62403_s_at	HUMIGFBP5	insulin-like growth factor bin	av dif pos
M62403_s_at	HUMIGFBP5	insulin-like growth factor bin	av dif pos
M62486_at	UMPRPC4S12	C4b-binding protein gene, exon	av dif pos
M63256_at	HUMCDR2AA	major Yo paraneoplastic antige	av dif pos
M63379_at	HUMTRPM2A4	TRPM-2 protein gene, exons 7,8	av dif pos
M63438_s_at	HUMIGGK	Ig rearranged gamma chain mRNA	av dif pos
M63438_s_at	HUMIGGK	Ig rearranged gamma chain mRNA	av dif pos
M63573_at	HUMSCYLP	secreted cyclophilin-like prot	av dif pos
M63589_at	HUMSCL7	stem cell leukemia gene produc	log neg
M64347_at	HUMFGFLR	novel growth factor receptor m	log neg
M64347_at	HUMFGFLR	novel growth factor receptor m	log neg
M64673_at	HUMHSF1	heat shock factor 1 (TCF5) m	log neg
M64716_at	HUMRPS25	ribosomal protein S25 mRNA, :	log neg
M64992_at	HUMPROS30	prosome protein P30-33K (pro	log neg
M65292_s_at	HUMHAAA	factor H homologue mRNA, :fa	log neg
M65292_s_at	HUMHAAA	factor H homologue mRNA, :fa	log neg
M66023_at	HUMGGEFERA	globin gene.	log neg
M66066_at	HUMMOESIN	moesin mRNA, :moesin :moesin	log neg
M66238_at	HUMARNTA	aryl hydrocarbon receptor nucl	log neg
M73077_at	HUMGRF1A	glucocorticoid receptor repres	log neg
M73239_s_at	HUMSCFA1	(clone SF1) hepatocyte growt	log neg
M73547_at	HUMPOLLA	polyposis locus (DP1 gene) m	log neg
M74093_at	HUMCLNC	cyclin mRNA. :cyclin E1	log neg
M74297_at	HUMHOX14	homeobox 1.4 protein mRNA, :h	log neg
M74715_s_at	HUMIDNAL	alpha-L-iduronidas (IDUA) mR	log neg
M77232_ma1_at	HUMRPS6B	ribosomal protein S6 gene, com	log neg
M77836_at	HUMP5CR	pyrroline 5-carboxylate reduct	log neg
M80244_at	HUME16GEN	E16 mRNA,	log neg
M80254_at	HUMCYP	cyclophilin isoform (hCyp3)	log neg
M80359_at	HUMP78A	protein p78 mRNA, :MAP/microt	log neg
M80563_at	HUMCAPL	CAPL protein mRNA, :S100 calc	log neg
M80563_at	HUMCAPL	CAPL protein mRNA, :S100 calc	log neg
M80899_at	HUMAHNAKA	novel protein AHNAK mRNA, part	log neg
M81750_at	HUMMCNDA	myeloid cell nuclear different	log neg
M81757_at	HUMS19RP	S19 ribosomal protein mRNA,	log neg
M81883_at	HUMGAD67A	glutamate decarboxylase (GAD6	log neg
M83181_at	HUMHTRB	serotonin receptor gene, :5-h	log neg
M84424_at	HUMCTSE09	cathepsin E (CTSE) gene, exo	log neg
M84711_at	HUMFTE1A	v-fos transformation effector	log neg
M85289_at	HUMHSPG2B	heparan sulfate proteoglycan	log neg
M86400_at	HUMPHPLA2	phospholipase A2 mRNA, :tyros	log neg
M86699_at	HUMTTK	kinase (TTK) mRNA, :TTK pro	log neg
M86737_at	HUMHMGBP	high mobility group box (SSRP	log neg
M87789_s_at	HUMIGHEPAH	(hybridoma H210) anti-hepati	log neg
M87789_s_at	HUMIGHEPAH	(hybridoma H210) anti-hepati	log neg
M90356_f_at	HUMBTFD	BTF3 protein homologue gene,	log neg
M90656_at	HUMGCSH	gamma-glutamylcysteine synthet	log neg

M91670_at	HUME2EP1	ubiquitin carrier protein \E2	log neg
M94856_at	HUMFABPHA	fatty acid binding protein hom	log neg
M94856_at	HUMFABPHA	fatty acid binding protein hom	log neg
M94880_f_at	HUMHLAAX	MHC class I \HLA-A*8001\ mRNA	log neg
M96233_s_at	HUMGSTM4A	glutathione transferase class	log neg
M96233_s_at	HUMGSTM4A	glutathione transferase class	log neg
M96326_ma1_at	HUMAZCDI	azurocidin gene,	log neg
M96956_at	HUMTDGF3A	\clone CR-3\ teratocarcinoma	log neg
M97796_s_at	HUMID2X	helix-loop-helix protein \Id-	log neg
M97815_at	HUMCRABP02	retinoic acid-binding protein	log neg
S34389_at	HMOX2	heme oxygenase-2 [human, kidney]	log neg
S58544_at	SPAG1	75 kDa infertility-related spe	log neg
S69115_at	S69115	granulocyte colony-stimulating	log neg
S69115_at	S69115	granulocyte colony-stimulating	log neg
S71043_ma1_s_at	S71043	Ig alpha 2=immunoglobulin A he	log neg
S71043_ma1_s_at	S71043	Ig alpha 2=immunoglobulin A he	log neg
S73591_at	VDUP1	brain-expressed HHCPA78 homolo	log neg
S73591_at	VDUP1	brain-expressed HHCPA78 homolo	log neg
S75463_at	S75463	P43=mitochondrial elongation f	log neg
S77356_at	S77356	transcript ch21=oligomycin sen	log neg
S77582_at	S77582	HERVK10/HUMMTV reverse transcr	log neg
S78234_at	S78234	nuc2 homolog [human, fibroblas	log neg
S78771_s_at	S78771	NAT=CpG island-associated gene	log neg
S79219_s_at	S79219	metastasis-associated gene [hu	log neg
S79522_at	S79522	ubiquitin carboxyl extension p	log neg
S80562_at	CNN3	acidic calponin [human, kidney]	log neg
S82297_at	S82297	beta 2-microglobulin {11bp del	log neg
S82597_ma1_s_at	S82597	UDP-GalNAc:polypeptide	log neg
S90469_at	POR	cytochrome P450 reductase [hum	log neg
U00947_s_at	U00947	clone C4E 3.2 \CAC\ n\ (GTG\)	log neg
U03397_s_at	U03397	receptor protein 4-1BB mRNA,	log neg
U03398_at	TNFSF9	receptor 4-1BB ligand mRNA, :	log neg
U04241_at	U04241	homolog of Drosophila enhancer	log neg
U04313_at	PI5	maspin mRNA, :protease inhibi	log neg
U05340_at	CDC20	p55CDC mRNA, :cell division c	log neg
U06155_s_at	U06155	chromosome 1q subtelomeric seq	log neg
U06863_at	U06863	folliculin-related protein pr	log neg
U06863_at	U06863	folliculin-related protein pr	log neg
U09117_at	PLCD1	phospholipase C delta 1 mRNA,	log neg
U09303_at	EFNB1	T cell leukemia LERK-2 \EPLG2	log neg
U09813_at	ATP5G3	mitochondrial ATP synthase sub	log neg
U09953_at	U09953	ribosomal protein L9 mRNA, :r	log neg
U10362_at	U10362	GP36b glycoprotein mRNA,	log neg
U10492_at	HSMOX1	Mox1 protein \MOX1\ mRNA, :	log neg
U12404_at	U12404	Csa-19 mRNA,	log neg
U12404_at	U12404	Csa-19 mRNA,	log neg
U12465_at	U12465	ribosomal protein L35 mRNA,	log neg
U12779_at	U12779	MAP kinase activated protein k	log neg
U14391_at	MYO1C	myosin-IC mRNA, :myosin IC	log neg
U14588_at	PXN	paxillin mRNA, :paxillin :pax	log neg
U14968_at	U14968	ribosomal protein L27a mRNA,	log neg
U14969_at	U14969	ribosomal protein L28 mRNA, :	log neg
U14970_at	U14970	ribosomal protein S5 mRNA, :r	log neg
U14971_at	U14971	ribosomal protein S9 mRNA, :r	log neg
U14971_at	U14971	ribosomal protein S9 mRNA, :r	log neg

U14972_at	U14972	ribosomal protein S10 mRNA,	log neg
U14973_at	U14973	ribosomal protein S29 mRNA, :	log neg
U15177_at	U15177	cosmid CRI-JC2015 at D10S289 I	log neg
U16860_at	ECH1	peroxisomal enoyl-CoA hydratase	log neg
U16799_s_at	U16799	Na,K-ATPase beta-1 subunit mRNA	log neg
U16861_at	KCNJ2	inward rectifying potassium ch	log neg
U17077_at	BENE	BENE mRNA, :BENE protein	log neg
U17760_ma1_at	HSLAMB3S17	laminin S B3 chain \(\Lambda MB3\)	log neg
U19247_ma1_s_at	HSINFGRA7	interferon-gamma receptor alph	log neg
U19251_s_at	NAIP	neuronal apoptosis inhibitory	log neg
U20657_at	USP4	ubiquitin protease \(\text{Unph}\)	log neg
U20734_s_at	U20734	transcription factor junB \(\text{ju}\)	log neg
U20734_s_at	U20734	transcription factor junB \(\text{ju}\)	log neg
U20758_ma1_at	U20758	osteopontin gene,	log neg
U22376_cds2_s_at	MYB	\(\text{c-myb}\)	log neg
U22431_s_at	U22431	hypoxia-inducible factor 1 alp	log neg
U22970_ma1_s_at	U22970	interferon-inducible peptide	log neg
U22970_ma1_s_at	U22970	interferon-inducible peptide	log neg
U24183_s_at	U24183	phosphofructokinase \(\text{PFKM}\)	log neg
U24389_s_at	HSLYOXL7	lysyl oxidase-like protein gen	log neg
U25789_at	U25789	ribosomal protein L21 mRNA, :	log neg
U27333_at	U27333	alpha \(\text{1,3}\)	log neg
U27333_at	U27333	alpha \(\text{1,3}\)	log neg
U27831_at	U27831	striatum-enriched phosphatase	log neg
U29175_at	U29175	transcriptional activator \(\text{BR}\)	log neg
U29953_ma1_at	PEDF	pigment epithelium-derived fac	log neg
U30827_s_at	U30827	splicing factor SRp40-3 \(\text{SRp4}\)	log neg
U30888_at	USP14	tRNA-guanine transglycosylase	log neg
U30888_at	USP14	tRNA-guanine transglycosylase	log neg
U31814_at	HDAC2	transcriptional regulator homo	log neg
U31875_at	HEP27	Hep27 protein mRNA, :short-ch	log neg
U32944_at	PIN	cytoplasmic dynein light chain	log neg
U34880_at	U34880	DPH2L mRNA, :DPH2L "mRNA," co	log neg
U36341_ma1_at	U36341	Xq28 cosmid, creatine transpor	log neg
U36764_at	U36764	TGF-beta receptor interacting	log neg
U37012_at	U37012	cleavage and polyadenylation s	log neg
U37146_at	U37146	silencing mediator of retinoid	log neg
U37408_at	CTBP1	phosphoprotein CtBP mRNA, :C-	log neg
U37689_at	POLR2H	RNA polymerase II subunit \(\text{hs}\)	log neg
U38276_at	SEMA3F	semaphorin III family homolog	log neg
U38276_at	SEMA3F	semaphorin III family homolog	log neg
U39400_at	C11orf4	NOF1 mRNA, :chromosome 11 op	log neg
U40998_at	U40998	retinal protein \(\text{HRG4}\)	log neg
U41060_at	U41060	breast cancer, estrogen regula	log neg
U41766_s_at	ADAM9	metalloprotease/disintegrin/cy	log neg
U42359_at	HUMN33S10	N33 protein form 1 \(\text{N33}\)	log neg
U43328_at	U43328	link protein mRNA,	log neg
U43901_ma1_s_at	U43901	37 kD laminin receptor precurs	log neg
U43901_ma1_s_at	U43901	37 kD laminin receptor precurs	log neg
U45448_s_at	U45448	P2x1 receptor mRNA,	log neg
U48705_ma1_s_at	U48705	receptor tyrosine kinase DDR g	log neg
U48936_at	U48936	amiloride-sensitive epithelial	log neg
U48936_at	U48936	amiloride-sensitive epithelial	log neg
U49395_at	U49395	ionotropic ATP receptor P2X5a	log neg
U49889_ma1_at	UBB	ubiquitin gene, :ubiquitin B	log neg

U50523_at	U50523	BRCA2 region, mRNA sequence CG	log neg
U50829_at	BHMT	betaine:homocysteine methyltra	log neg
U52154_at	KCNJ5	G protein-coupled inwardly rec	log neg
U52154_at	KCNJ5	G protein-coupled inwardly rec	log neg
U52696_s_at	U52696	adrenal Creb-rp homolog \(\Creb	log neg
U53786_at	U53786	envoplakin \(\EVPL\) mRNA, :en	log neg
U55054_at	HSKCC	K-Cl cotransporter \(\hKCC1\) m	log neg
U55054_at	HSKCC	K-Cl cotransporter \(\hKCC1\) m	log neg
U57341_r_at	U57341	neurofilament triplet L protei	log neg
U57342_at	MLF2	myelodysplasia/myeloid leukemi	log neg
U57629_at	RPGR	retinitis pigmentosa GTPase re	log neg
U58682_at	U58682	ribosomal protein S28 mRNA, :	log neg
U60975_at	U60975	hybrid receptor gp250 precurs	log neg
U60975_at	U60975	hybrid receptor gp250 precurs	log neg
U62739_at	BCAT2	branched-chain amino acid amin	log neg
U62962_at	EIF3S6	Int-6 mRNA, :eukaryotic trans	log neg
U63541_at	U63541	mRNA expressed in HC/HCC liver	log neg
U64863_at	PDCD1	hPD-1 \(\hPD-1\) mRNA, :progra	log neg
U66061_cds3_at	U66061	germline T-cell receptor beta	log neg
U66406_at	EFNB3	putative EPH-related PTK recep	log neg
U66616_at	SMARCC2	SWI/SNF complex 170 KDa subuni	log neg
U66616_at	SMARCC2	SWI/SNF complex 170 KDa subuni	log neg
U67092_s_at	U67092	ataxia-telangiectasia locus pr	log neg
U67156_at	MEKK5	mitogen-activated kinase kinas	log neg
U68105_s_at	HSPABPS13	poly(A)-binding protein \(\PA	log neg
U70732_ma1_at	GPT	glutamate pyruvate transaminas	log neg
U70867_at	SLC21A2	prostaglandin transporter hPGT	log neg
U73379_at	U73379	cyclin-selective ubiquitin car	log neg
U73379_at	U73379	cyclin-selective ubiquitin car	log neg
U73824_at	EIF4G2	p97 mRNA, :eukaryotic transla	log neg
U73843_at	U73843	epithelial-specific transcript	log neg
U77456_at	NAP1L4	nucleosome assembly protein 2	log neg
U77846_ma1_at	U77846	elastin gene, partial cds and	log neg
U77846_ma1_s_at	U77846	elastin gene, partial cds and	log neg
U77846_ma1_s_at	U77846	elastin gene, partial cds and	log neg
U78027_ma3_at	U78027	Bruton's tyrosine kinase \(\BTK	log neg
U78095_at	U78095	placental bikunin mRNA, :Plac	log neg
U78678_at	U78678	thioredoxin mRNA, nuclear gene	log neg
U78722_at	U78722	zinc finger protein 165 \(\Zpf1	log neg
U78735_at	U78735	ABC3 mRNA,	log neg
U79256_at	U79256	clone 23719 mRNA sequence.	log neg
U79280_at	U79280	clone 23575 mRNA,	log neg
U79299_at	U79299	neuronal olfactomedin-related	log neg
U80184_ma1_at	FLII	FLII gene, :flightless I \(\Dr	log neg
U81984_at	EPAS1	endothelial PAS domain protein	log neg
U82169_at	FZD9	frizzled homolog \(\FZD3\) mRNA	log neg
U82169_at	FZD9	frizzled homolog \(\FZD3\) mRNA	log neg
U82818_at	U82818	UCP3S mRNA,	log neg
U83246_at	CPNE1	copine I mRNA, :copine I :cop	log neg
U83598_at	U83598	death domain receptor 3 solubl	log neg
U86136_at	U86136	telomerase-associated protein	log neg
U87972_at	U87972	NAD+-isocitrate dehydrogenase	log pos
U88964_at	ISG20	HEM45 mRNA, :interferon stimu	log pos
U89326_at	U89326	bone morphogenetic protein rec	log pos
U90426_at	DDXL	nuclear RNA helicase, :nuclea	log pos

U90552_s_at	U90552	butyrophilin (BTF5) mRNA, :	log pos
U90913_at	U90913	clone 23665 mRNA sequence. :cl	log pos
U90916_at	U90916	clone 23815 mRNA sequence. :cl	log pos
U94747_at	HAN11	WD repeat protein HAN11 mRNA,	log pos
U95740_ma1_at	U95740	Chromosome 16 BAC clone CIT987	log pos
V00571_ma1_at	HSPCRF	gene encoding prepro form of c	log pos
V00572_at	HSPGK1	mRNA encoding phosphoglycerate	log pos
V00594_s_at	HSTHIO	metallothionein from cadmium-	log pos
V01512_ma1_at	HSCFOS	cellular oncogene c-fos (comp	log pos
X00274_at	HSHL07	gene for HLA-DR alpha heavy ch	log pos
X00274_at	HSHL07	gene for HLA-DR alpha heavy ch	log pos
X00351_f_at	HSAC07	beta-actin.	log pos
X00368_xpt2_at	HSPROL1	prolactin gene 5' region.	log pos
X01677_f_at	HSGAPDR	liver glyceraldehyde-3-phosph	log pos
X02152_at	HSLDHAR	lactate dehydrogenase-A (LDH	log pos
X02596_at	HSBCRR	bcr (breakpoint cluster regi	log pos
X03068_f_at	HSHLDQWB	HLA-D class II antigen DQw1.1	log pos
X03100_cds2_at	HSHLASBA	HLA-SB(DP) alpha gene. :HLA-	log pos
X03100_cds2_at	HSHLASBA	HLA-SB(DP) alpha gene. :HLA-	log pos
X03342_at	HSRPL32	ribosomal protein L32. :ribos	log pos
X03689_s_at	HSEFTUR5	mRNA fragment for elongation f	log pos
X03689_s_at	HSEFTUR5	mRNA fragment for elongation f	log pos
X04347_s_at	HSUPIR1	liver mRNA fragment DNA bindin	log pos
X04347_s_at	HSUPIR1	liver mRNA fragment DNA bindin	log pos
X06614_at	HSRRA	receptor of retinoic acid. :r	log pos
X06617_at	HSRPS11	ribosomal protein S11. :ribo	log pos
X06985_at	HSOXYGR	heme oxygenase. :heme oxygena	log pos
X06985_at	HSOXYGR	heme oxygenase. :heme oxygena	log pos
X07696_at	HSKERC15	cytokeratin 15. :keratin 15 :	log pos
X07730_at	HSPSA	prostate specific antigen. :	log pos
X07730_at	HSPSA	prostate specific antigen. :	log pos
X12447_at	HSALDOA	aldolase A gene (EC 4.1.2.13	log pos
X12671_ma1_at	HSHNRNPA	gene for heterogeneous nuclear	log pos
X12671_ma1_at	HSHNRNPA	gene for heterogeneous nuclear	log pos
X12876_s_at	HSKER18A	mRNA fragment for cytokeratin	log pos
X12876_s_at	HSKER18A	mRNA fragment for cytokeratin	log pos
X13334_at	HSCD14R	CD14 myeloid cell-specific leu	log pos
X13546_ma1_at	HSHMG17G	HMG-17 gene for non-histone ch	log pos
X13794_ma1_at	HSLDHB1	lactate dehydrogenase B gene e	log pos
X13794_ma1_at	HSLDHB1	lactate dehydrogenase B gene e	log pos
X14008_ma1_f_at	HSLYSOZY	lysozyme gene (EC 3.2.1.17).	log pos
X15940_at	HSRPL31	ribosomal protein L31. :ribos	log pos
X16064_at	HSTUMP	translationally controlled tu	log pos
X16832_at	HSCATHH	cathepsin H (EC 3.4.22.16).	log pos
X17042_at	HSHPCP	hematopoietic proteoglycan cor	log pos
X17206_at	HSLREP3	LLRep3. : LLRep3	log pos
X51345_at	HSJUNB	jun-B JUN-B protein. :jun B p	log pos
X51466_at	HSEF2	elongation factor 2. : elonga	log pos
X51688_at	HSCYCLINA	cyclin A.	log pos
X52003_at	HSPS2MKN	pS2 protein gene. :trefoil fac	log pos
X52003_at	HSPS2MKN	pS2 protein gene. :trefoil fac	log pos
X52426_s_at	HSCYTK	cytokeratin 13. : cytokeratin	log pos
X52426_s_at	HSCYTK	cytokeratin 13. : cytokeratin	log pos
X52851_ma1_at	HSCPH70	cyclophilin gene for cyclophil	log pos
X52966_at	HSL35A	ribosomal protein L35a. :ribo	log pos

X53586_ma1_at	HSINTA8R	integrin alpha 6. :integrin,	log pos
X53587_at	HSINTB4R	integrin beta 4. : integrin b	log pos
X53777_at	HSL23MR	L23 putative ribosomal protel	log pos
X54232_at	HSGLYPIC	heparan sulfate proteoglycan	log pos
X54667_at	HSCYSTATS	cystatin S.	log pos
X54942_at	HSCKSHS2	ckshs2 Cks1 protein homologue	log pos
X54942_at	HSCKSHS2	ckshs2 Cks1 protein homologue	log pos
X55005_ma1_at	HSCERBAR	c-erbA-1 thyroid hormone rece	log pos
X55715_at	HSUMS3	Hums3 40S ribosomal protein s	log pos
X55954_at	HSL17ARP	HL23 ribosomal protein homolo	log pos
X56494_at	HSPKM12	M gene for M1-type and M2-type	log pos
X56687_s_at	HSAUTNOR	autoantigen NOR-90.	log pos
X56807_at	HSDGII	DSC2 desmocollins type 2a and	log pos
X56841_at	HSHLAE	HLA-E gene. :major histocompat	log pos
X56932_at	HS23KDHP	23 kD highly basic protein.	log pos
X57351_at	HS18D	1-8D gene from interferon-indu	log pos
X57351_at	HS18D	1-8D gene from interferon-indu	log pos
X57351_s_at	HS18D	1-8D gene from interferon-indu.	log pos
X57809_s_at	HSIGVL009	rearranged immunoglobulin lamb	log pos
X57809_s_at	HSIGVL009	rearranged immunoglobulin lamb	log pos
X57959_at	HSRBPRL7A	ribosomal protein L7. :riboso	log pos
X58072_at	HSGATA3R	hGATA3 trans-acting T-cell sp	log pos
X59373_at	HSHOX4D	HOX4D a homeobox protein. :ho	log pos
X59798_at	HSPRAD1CY	PRAD1 cyclin. :PRAD1 cyclin	log pos
X60489_at	HSEF1B	elongation factor-1-beta.	log pos
X61587_at	HSRHOG	rhoG GTPase. :ras homolog gen	log pos
X62320_at	HSEPIT1	epithelin 1 and 2. : epitheli	log pos
X62466_at	HSCAMPAT1	CAMPATH-1 \(\text{CDw52}\) antigen.	log pos
X62466_at	HSCAMPAT1	CAMPATH-1 \(\text{CDw52}\) antigen.	log pos
X62654_ma1_at	HSMECDAG	gene for Me491/CD63 antigen. :	log pos
X62691_at	HSRPRNA	ribosomal protein \(\text{homologuo}	log pos
X63359_at	HSUGT2BIO	UGT2BIO udp glucuronosyltrans	log pos
X63527_at	HSRPL19	ribosomal protein L19. :ribos	log pos
X63629_at	HSPCAD	p cadherin. :cadherin 3, P-ca	log pos
X64229_at	HSDEK9	dek mRNA. :DEK gene	log pos
X64707_at	HSBBC1	BBC1 mRNA.	log pos
X65614_at	HSS100PCB	calcium-binding protein S100P	log pos
X66114_ma1_at	HS2OXOC	gene for 2-oxoglutarate carrie	log pos
X66363_at	HSSTHPKD	mRNA PCTAIRE-1 for serine/thre	log pos
X66363_at	HSSTHPKD	mRNA PCTAIRE-1 for serine/thre	log pos
X66699_at	HSEWS	EWS mRNA. :Ewing sarcoma break	log pos
X67247_ma1_at	HSRPS8	rpS8 gene for ribosomal protel	log pos
X67325_at	HSP27	p27 mRNA. :interferon, alpha-i	log pos
X67951_at	HSPAG	proliferation-associated gene	log pos
X68314_at	HSQPGI	glutathione peroxidase-GI. :g	log pos
X68314_at	HSQPGI	glutathione peroxidase-GI. :g	log pos
X68688_ma1_s_at	HSZNB	ZNF33B gene.	log pos
X69150_at	HSRPS18	ribosomal protein S18. :ribos	log pos
X69391_at	HSRPL8AA	ribosomal protein L8. :riboso	log pos
X69550_at	HSRHO1	rho GDP-dissociation inhibito	log pos
X69654_at	HSS26	ribosomal protein S26.	log pos
X70940_s_at	HSEFAC1A2	elongation factor 1 alpha-2.	log pos
X70940_s_at	HSEFAC1A2	elongation factor 1 alpha-2.	log pos
X73079_at	HSPIR	encoding Polymeric immunoglobu	log pos
X73358_s_at	HSAES1	hAES-1 mRNA. :amino-terminal e	log pos

X73460_at	HSRPL3A	ribosomal protein L3.	log pos
X73478_at	HSPTPAA	hPTPA mRNA. :hPTPA mRNA	log pos
X74819_at	HSCARTROT	cardiac troponin T.	log pos
X74819_at	HSCARTROT	cardiac troponin T.	log pos
X74929_s_at	HSKRT8	KRT8 keratin 8. :keratin 8 :K	log pos
X75252_at	HSPEABP	phosphatidylethanolamine bindi	log pos
X76534_at	HSNMB	NMB mRNA. :transmembrane glyco	log pos
X76534_at	HSNMB	NMB mRNA. :transmembrane glyco	log pos
X77794_at	HSCYCG1	cyclin G1. : cyclin G1	log pos
X78992_at	HSERF2	ERF-2 mRNA.	log pos
X79234_at	HSRPL11	ribosomal protein L11.	log pos
X79439_at	HSNOTCH3	Notch 3 DNA sequence. :Notch	log pos
X80062_at	HSSAMRNA	SA mRNA.	log pos
X80198_at	HSMLN64	MLN64 mRNA.	log pos
X80200_at	HSMLN62	MLN62 mRNA. :TNF receptor-asso	log pos
X80822_at	HSPLORF	ORF.	log pos
X80909_at	HSANAC	alpha NAC mRNA. :nascent-polyp	log pos
X82693_at	HSE48	E48 antigen. : E48 antigen	log pos
X82693_at	HSE48	E48 antigen. : E48 antigen	log pos
X83416_s_at	HSPRP2	PrP gene, exon 2. : "PrP "gene	log pos
X83492_at	HSFAS47	Fas/Apo-1 \clone pCRTM11-Fas	log pos
X83492_at	HSFAS47	Fas/Apo-1 \clone pCRTM11-Fas	log pos
X83572_at	HSARSD	ARSD gene, complete CDS. :aryl	log pos
X86809_at	HSPEA15	major astrocytic phosphoprote	log pos
X87159_at	HSSCNN1B	beta subunit of epithelial am	log pos
X87241_at	HSHFATPRO	hFat protein. :FAT tumor supp	log pos
X89416_at	HSRNAPPP5	protein phosphatase 5. :prote	log pos
X89416_at	HSRNAPPP5	protein phosphatase 5. :prote	log pos
X90846_at	HARNAMLK2	mixed lineage kinase 2.	log pos
X91103_at	HSRNAHR44	Hr44 protein.	log pos
X93036_at	HSMAT82	MAT8 protein. :phospholemman-	log pos
X94583_xp12_r_at	HSDBIEX12	dbi/acbp gene exon 1 & 2.	log pos
X94612_at	HS2CGMPPK	type II cGMP-dependent protei	log pos
X95404_at	HSNMCFL1	non-muscle type cofilin. :cof	log pos
X95735_at	HSZYXIN2R	zyxin. :zyxin	log pos
X95808_s_at	HSDXS	protein encoded by a candidat	log pos
X98482_at	HSTNNTX11	TNNT2 gene exon 11.	log pos
X98482_r_at	HSTNNTX11	TNNT2 gene exon 11.	log pos
X98482_r_at	HSTNNTX11	TNNT2 gene exon 11.	log pos
X98534_s_at	HSVASP413	VASP gene, exons 4 to 13. : "VA	log pos
X99133_at	HSNGALGEN	NGAL gene. :lipocalin 2 \onco	log pos
X99888_at	HSTYL	mRNA from TYL gene. :pleckstrl	log pos
Y00062_at	HSLCA	T200 leukocyte common antigen	log pos
Y00503_at	HSKER19	keratin 19. :keratin 19 : ker	log pos
Y00705_at	HSPSTI	pstl pancreatic secretory inh	log pos
Y00787_s_at	HSMDNCF	MDNCF \monocyte-derived neut	log pos
Y00787_s_at	HSMDNCF	MDNCF \monocyte-derived neut	log pos
Y00796_at	HSFLA1A	leukocyte-associated molecule	log pos
Y07755_at	HSS100A2	S100A2 gene, exon 1, 2 and 3.	log pos
Y07755_at	HSS100A2	S100A2 gene, exon 1, 2 and 3.	log pos
Y08374_ma1_at	Y08374	gene encoding cartilage GP-39	log pos
Y08639_at	HSTFAC	nuclear orphan receptor ROR-b	log pos
Y08976_at	HSRNAFEV	FEV protein.	log pos
Y10207_at	HSCD171	CD171 protein.	log pos
Y10871_at	HSTWISTGE	twist gene. :twist \Drosophil	log pos

Y12670_at	HSOBRGRP	leptin receptor gene-related	log pos
Z12962_at	HSRPL41	homologue to yeast ribosomal	log pos
Z19554_s_at	HSVIMENTA	vimentin gene. :vimentin gene	log pos
Z19574_ma1_at	HSCYTOK17	gene for cytokeratin 17. :gene	log pos
Z22551_at	HSKINEC	kinectin gene.	log pos
Z25749_ma1_at	HSRPS7	gene for ribosomal protein S7.	log pos
Z25884_at	HSCLC1MR	CIC-1 muscle chloride channel	log pos
Z25884_at	HSCLC1MR	CIC-1 muscle chloride channel	log pos
Z28491_s_at	HSCOMT2	gene for catechol O-methyltran	log pos
Z28407_at	HSRBPL8	ribosomal protein L8. :riboso	log pos
Z28407_at	HSRBPL8	ribosomal protein L8. :riboso	log pos
Z30643_at	HSCLCHPRA	chloride channel \ (putative)	log pos
Z32765_at	HSCD38G15	CD38 gene exon 15.	log pos
Z35402_ma1_s_at	HSECAD3	gene encoding E-cadherin, exon	log pos
Z35402_ma1_s_at	HSECAD3	gene encoding E-cadherin, exon	log pos
Z48501_s_at	HSPABPII	polyadenylate binding protein	log pos
Z48950_at	HSHH3X3B	hH3.3B gene for histone H3.3.	log pos
Z49107_s_at	Z49107	galectin.	log pos
Z49148_s_at	HSRPL29	ribosomal protein L29.	log pos
Z49148_s_at	HSRPL29	ribosomal protein L29.	log pos
Z49835_s_at	HSP2SISOM	protein disulfide isomerase.	log pos
Z50022_at	HSSGP1N15	surface glycoprotein. :chromo	log pos
Z69043_s_at	HSTRAPRNA	mRNA translocon-associated pro	log pos
Z70759_at	HSM243	mitochondrial 16S rRNA gene \ (log pos
Z80783_at	HSH2BL	H2B/ gene. :H2B histone famil	log pos
Z80787_at	HSH4J	H4/ gene. :H4 histone family,	log pos
Z80787_at	HSH4J	H4/ gene. :H4 histone family,	log pos
Z83804_at	HSHDHC7	axonemal dynein heavy chain	log pos
Z84721_cds2_at	HSGG1	DNA sequence from cosmid GG1 f	log pos
Z84721_cds2_at	HSGG1	DNA sequence from cosmid GG1 f	log pos
Z93784_at	HS398C22	DNA sequence from PAC 398C22 o	log pos

TABLE 10

Urothelium			Other cell types			
Protein	Normal	pTa	pT2+	Leukocytes	Endothelium	Histiocytes
					m	
Keratin 8	+	+	+	-	-	-
CystatinC	+	+	+	+		+
Vimentin	+	-	+		+	
E-cadherin	+	(+)	(+)	?		
CD59	+	(+)	-	+	+	+
					+	
Cathepsin E	-	+	-	+		+
junB	-	+	-	-	-	+
IGF	+	+	-	-	-	-
Beta-2-microglob.	+	+	+	+	+	-
ApoE	+	-	+	-	-	-

CLAIMS

1. A method of determining an expression pattern of a cell sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present, comprising:
5 determining expression of one or more genes in a sample comprising cells, wherein the one or more genes excludes genes which are expressed in the submucosal, smooth muscle, or connective tissue, whereby a pattern of expression is formed for the sample which is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the sample.
- 10 2. The method of claim 1 wherein the sample comprises epithelial or carcinoma cells.
3. The method of claim 2 wherein the sample comprises urothelial or bladder cancer cells.
- 15 4. A method of determining an expression pattern of a cell sample, comprising:
determining expression of one or more genes in a sample comprising cells, whereby a first pattern of expression is formed for the sample;
removing expression of genes which are expressed in submucosal, smooth muscle, or connective tissue cells from the first pattern of expression,
20 whereby a second pattern of expression is formed, wherein the second pattern is independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the sample.
5. The method of claim 4 wherein the cell sample is an epithelium or carcinoma sample.
- 25 6. The method of claim 5 wherein the cell sample is a urothelium or bladder cancer sample.
7. A method for determining an expression pattern of a urothelium or bladder cancer cell, comprising:
determining expression of one or more genes in a sample comprising
30 urothelium or bladder cancer cells, whereby a first pattern of expression is formed;

subtracting from the first pattern of expression a second pattern of expression, wherein the second pattern was formed using the one or more genes and a sample comprising predominantly submucosal, smooth muscle, or connective tissue cells, said step of subtracting forming a third pattern of expression which reflects expression of the urothelium or bladder cancer cells independent of the proportion of submucosal, smooth muscle, or connective tissue cells present in the sample.

8. A method of detecting an invasive tumor in a patient, comprising:

detecting in a sample of a body fluid a marker which is more prevalent in submucosal, smooth muscle, or connective tissue than in the body fluid, wherein the marker is an mRNA or protein expression product of a gene, wherein an increased amount of the marker in the body fluid indicates a tumor which has become invasive in the patient.

9. The method of claim 8 wherein the body fluid is selected from the group consisting of blood, plasma, serum, urine, ascites fluid, pleural fluid, spinal fluid, sputum, and mucous secretions.

10. The method of claim 8 wherein the marker is a protein characteristic of submucosal, smooth muscle, or connective tissue, but not found in the body fluid.

11. A method to diagnose a bladder cancer comprising:

determining a first pattern of expression of one or more genes in a bladder tissue sample suspected of being neoplastic;

comparing the first pattern of expression to a second and third reference pattern of expression, wherein the second pattern is of the one or more genes in normal urothelium and the third pattern is of the one or more genes in bladder cancer, wherein a first pattern of expression which is more similar to the third pattern than the second indicates neoplasia of the bladder tissue sample.

12. A method to predict outcome or prescribe treatment of a bladder tumor, comprising:

determining a first pattern of expression of one or more genes in a bladder tumor sample;

5 comparing the first pattern to one or more reference patterns of expression determined for bladder tumors at grades I to IV;

determining which of the reference patterns shares maximum similarity with the first pattern, wherein the outcome or treatment appropriate for the grade of tumor of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

10 13. A method to determine grade of a bladder tumor, comprising:
determining a first pattern of expression of one or more genes in a bladder tumor sample;

15 comparing the first pattern to one or more reference patterns of expression determined for bladder tumors at grades I to IV;

determining which of the reference patterns shares maximum similarity with the first pattern, wherein the grade of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

20 14. A method to determine stage of a bladder tumor, comprising:
determining a first pattern of expression of one or more genes in a bladder tumor sample;

comparing the first pattern to one or more stage-specific reference patterns;

25 determining which of the stage-specific reference patterns shares maximum similarity with the first pattern, wherein the stage of the reference pattern with the maximum similarity is assigned to the bladder tumor sample.

30 15. The method of claim 14 wherein the pattern of expression of the bladder tumor sample and the reference patterns comprise data on the expression of one or more genes selected from the group consisting of TCC-related genes, bladder papilloma-related genes, and invasive TCC-related genes.

16. A method of identifying a tissue sample as urothelial,
comprising:

determining a first pattern of expression of one or more genes in a
tissue sample;

5 comparing the first pattern of expression to a second pattern of
expression obtained from normal urothelial cells; wherein similarity between
the first and second patterns identifies the tissue sample as urothelial in its
origin.

17. The method of claim 16 further comprising the step of:
10 comparing the first pattern to one or more third patterns of expression
obtained from other cell types, wherein differences between the first
and third patterns confirms the suggestion that the tissue sample is
urothelial in origin.

18. A method to identify a set of genes useful for diagnosing,
15 predicting outcome, or prescribing treatment of a bladder
cancer comprising:

determining a first pattern of expression of one or more genes in a first
bladder tissue sample;

20 determining a second pattern of expression of the one or more genes
in a second bladder tissue sample, wherein the first bladder tissue sample is a
normal urothelium sample or an earlier stage or lower grade of bladder tumor
than the second bladder tissue sample;

25 comparing the first pattern of expression to the second pattern of
expression to identify a first set of genes whose expression is increased or
decreased in the second bladder tissue sample relative to the first bladder tissue
sample;

30 removing from the first set of genes those genes which are expressed
in submucosal, smooth muscle or connective tissue to produce a second set of
genes, wherein measurement of expression of the second set of genes can be
used for diagnosing, predicting outcome, or prescribing treatment of a bladder
cancer.

19. A method of determining an expression pattern of a bladder tissue sample independent of the proportion of submucosal, smooth muscle, or connective tissue cells present, comprising:
isolating a single-cell suspension of disaggregated bladder tumor cells
5 from a bladder tissue sample comprising bladder cells, and cells of one or more of a cell type selected from the group consisting of submucosal cells, smooth muscle cells, or connective tissue cells;
determining expression of one or more genes in the single-cell suspension, whereby a pattern of expression is formed for the sample which is
10 independent of the proportion of submucosal, smooth muscle, or connective tissue cells in the bladder tissue sample.
20. The method of any of claims 1-19 wherein expression of a gene is determined by assaying for an mRNA transcribed from the gene or a protein translated from an mRNA transcribed from the gene.
15
21. The method of any of claims 1-19 wherein expression of a plurality of genes is determined.
22. A method of screening for candidate therapeutic agents for treating bladder cancer, comprising the steps of:
20 contacting bladder tumor cells with a test compound;
determining gene expression of one or more genes in the bladder tumor cells which have been contacted with the test compound, wherein expression of the one or more genes changes during the development of a bladder cancer;
identifying a test compound as a candidate therapeutic agent if it causes
25 gene expression of at least one of the one or more genes to change to a level which is characteristic of an earlier stage of cancer progression.
23. A method of categorizing a tumor, comprising the steps of:
mixing cells of a plurality of tumors, wherein the tumors are of a single type and of a similar stage or grade to form a pool;
30 determining expression of one or more genes in the pool;

comparing expression of the one or more genes in the pool to expression in a test sample derived from a tumor, wherein similarities between the test sample expression and the pool expression permit categorization of the tumor.

- 5 24. A method of categorizing a tumor, comprising the steps of:
 mixing one or more gene products from cells of a plurality of
tumors, wherein the tumors are of a single type and of a similar stage or grade
to form a pool, wherein the gene product is mRNA or protein;
 determining expression of one or more genes in the pool by
10 assaying the gene product in the pool;

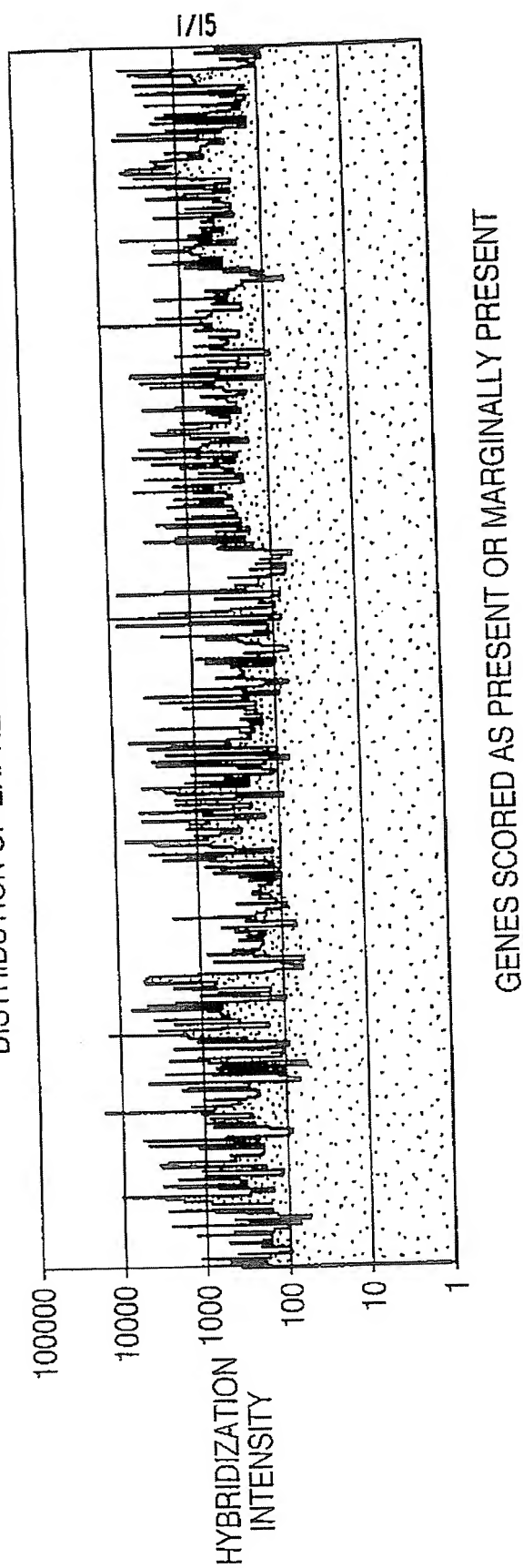
 comparing expression of the one or more genes in the pool to
expression in a test sample derived from a tumor, wherein similarities between
the test sample expression and the pool expression permit categorization of the
tumor.

- 15 25. A method of categorizing a tumor, comprising the steps of:
 determining expression of one or more genes in a plurality of
tumors, wherein the tumors are of a single type and of a similar stage or grade;
 combining data determined for the expression of the one or
more genes to form a data pool;
20 comparing expression of the one or more genes in the data pool
to expression in a test sample derived from a tumor, wherein similarities
between the test sample expression and the data pool permit categorization of
the tumor.

- 25 26. The method of claim 23, 24, or 25 wherein the tumors are
 bladder tumors.

FIG. 1

DISTRIBUTION OF EXPRESSION LEVELS IN BLADDER WALL

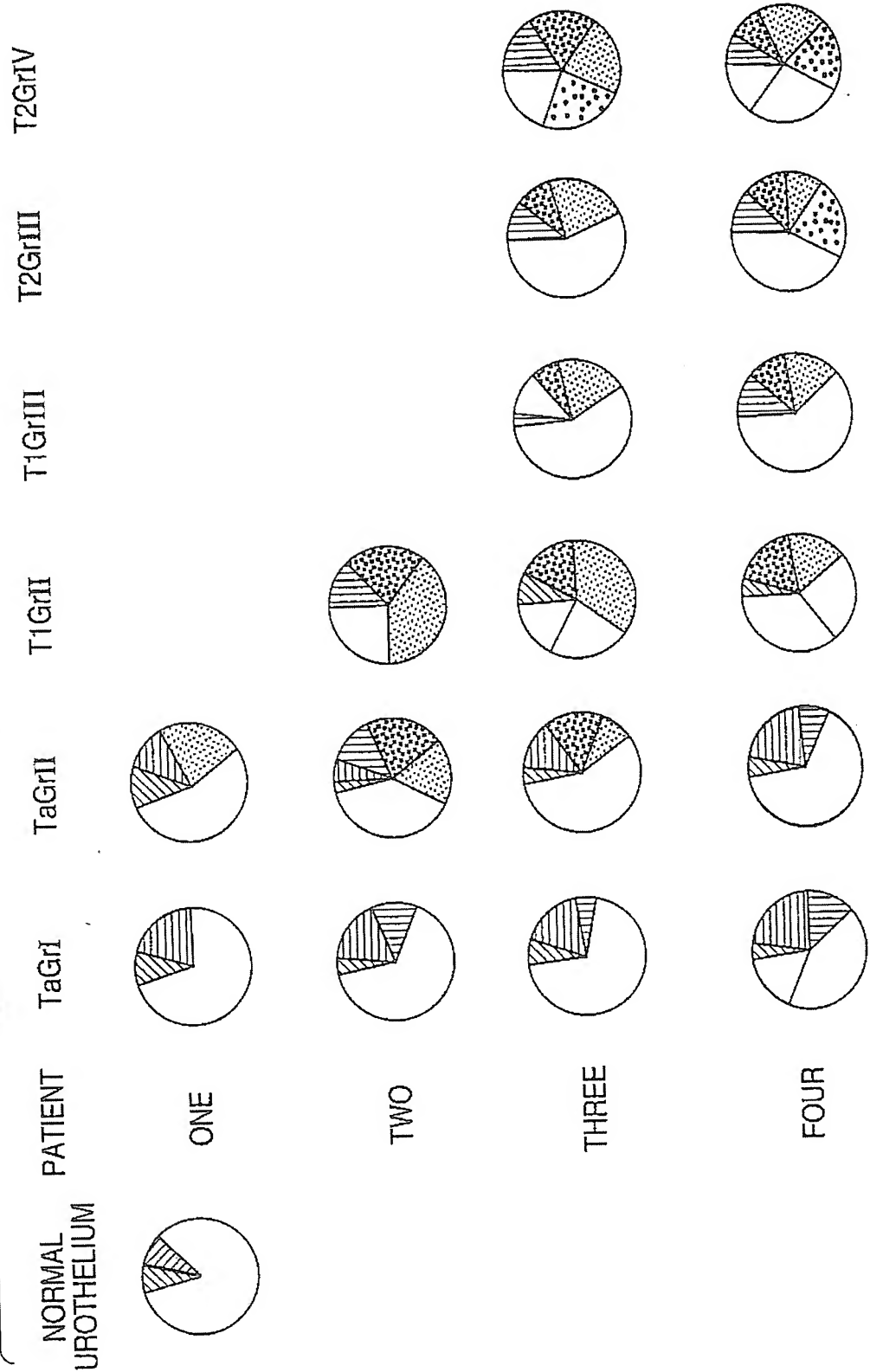


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Fig. 2 was missing at the time of publication

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FIG.3



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FIG. 4A

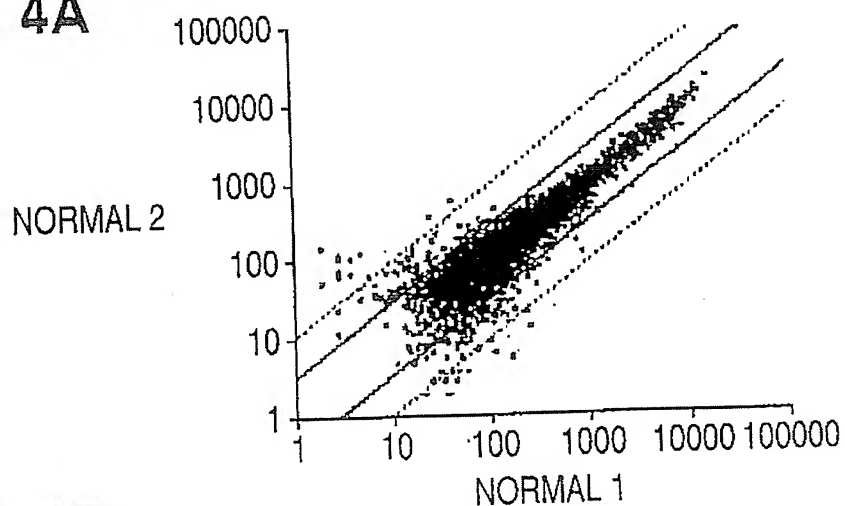


FIG. 4B

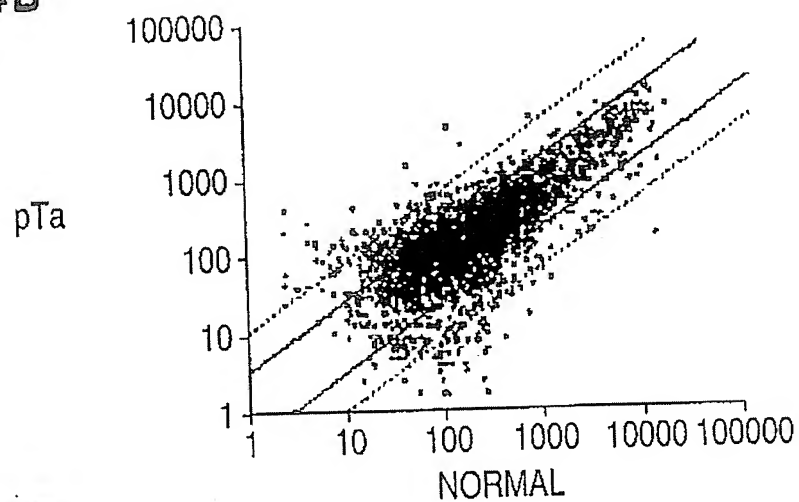
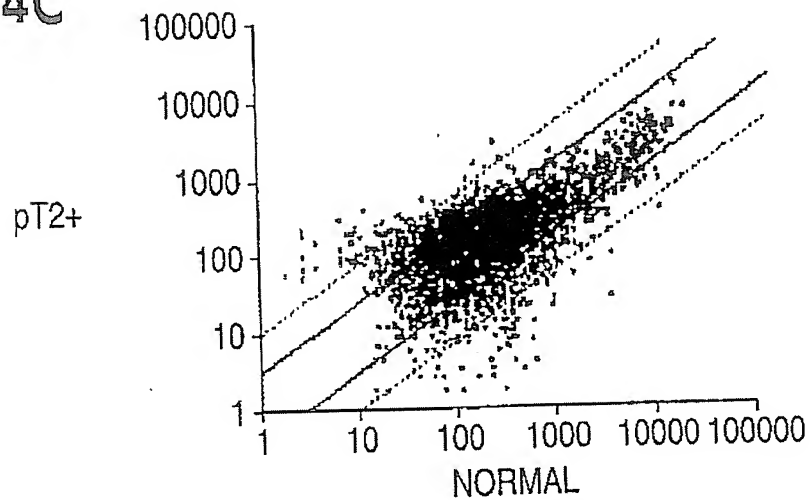


FIG. 4C



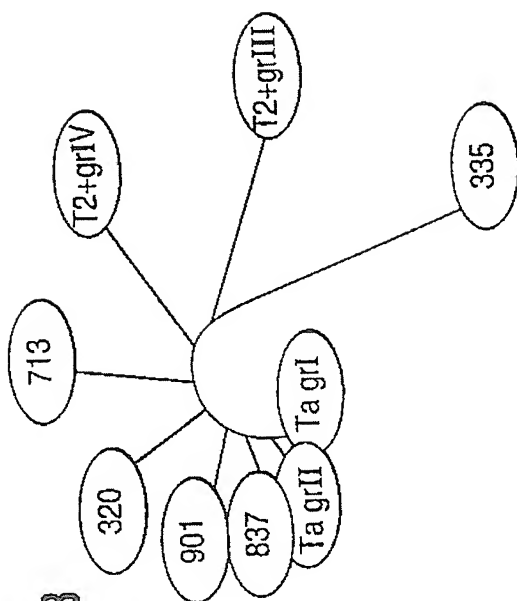


FIG. 5B

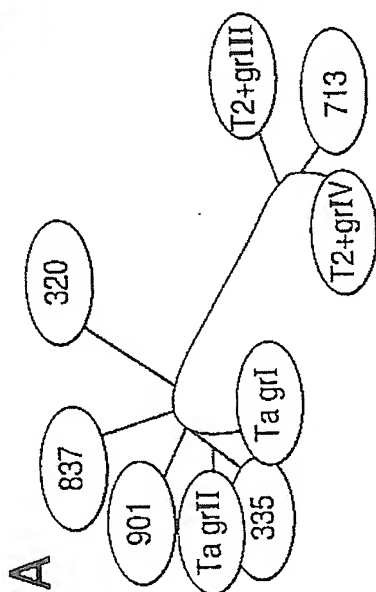


FIG. 5A

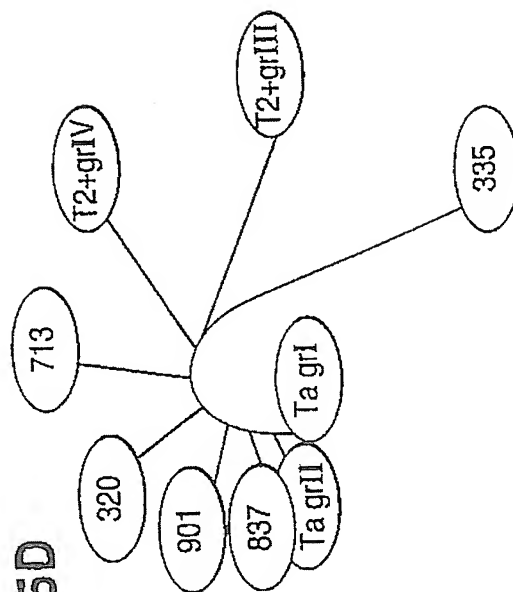


FIG. 5D

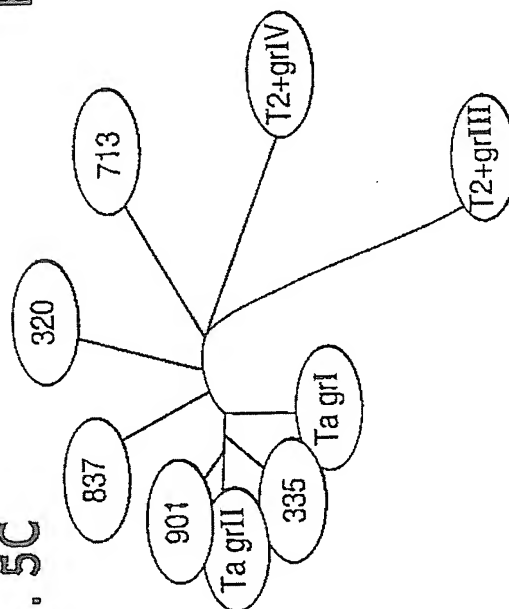
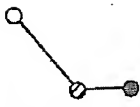


FIG. 5C

FIG. 6A

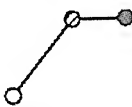
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TCC related genes



A.

M12125	Tropomyosin
D00654	Smooth muscle gamma-Actin
X04470	Antileukoprotease (ALP)
U08021	Nicotinamide N-methyltransferase (NNMT)
M16276	MHC class II HLA-DR2-Dw12
K02765	Complement component C3
J02854	Myosin light chain (MLC-2)
J05582	Pancreatic mucin
D17408	Calponin
M95787	Smooth muscle protein (SM22)
X99133	NGAL gene
M31951	Perforin (PRF1)
HG3431-HT3616	Decorin
S75256	Neutrophil lipocalin (HNL)
X13839	Smooth muscle alpha-Actin
M84526	Adipsin/complement factor D
AF001548	Chromosome 16 BAC clone CIT987SK-815A9

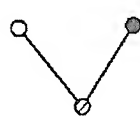
FIG. 6B



B.

M13955	Keratin K7 (type II)
D87953	RTP
HG3543-HT3739	Insulin-Like Growth Factor 2

FIG. 6C



Bladder papilloma related genes

C.

M63438	Ig rearranged gamma chain V-J-C region and complete cds
M25079	Sickle cell beta-globin
Z84721	Human DNA sequence 2Mb contig from cosmid GG1
X00274	HLA-DR alpha heavy chain a class II antigen
X57809	Rearranged immunoglobulin lambda light chain
M34516	Human omega light chain protein 14.1
M13560	Ia-associated invariant gamma-chain gene
L02326	Clone Hu lambda-17
M33600	MHC class II HLA-DR-beta-1 (HLA-DRB1)
HG1428-HT1428	"Globin Beta"
V00594	Metallothionein
X57351	1-8D gene from interferon-inducible gene family
S71043	Ig alpha 2=immunoglobulin A heavy chain allotype 2
M87789	"Human (hybridoma H210) anti-hepatitis A IgG
M12529	Human apolipoprotein E
HG3576-HT3779	MHC Class II Beta W52
M57466	MHC class II HLA-DP light chain
Z19554	Vimentin gene
X03068	HLA-D class II antigen DQw1.1 beta chain
J04164	Interferon-inducible protein 27-Sep
X17042	MRNA for hematopoietic proteoglycan core protein
M55998	Alpha-1 collagen type I

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FIG. 6D

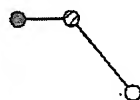


J03242
U20734
X64364
L12711
M32053
M17863
X15573
M22430
M84424
X59798
X07696
M94856

D.

Insulin-like growth factor II
Transcription factor junB
MRNA for M6 antigen
Transketolase (tk)
H19 RNA "gene"
Preproinsulin-like growth factor II (IGF-II)
Liver-type 1-phosphofructokinase (PFKL)
RASf-A PLA2
Cathepsin E (CTSE)
PRAD1 mRNA for cyclin
MRNA for cytokeratin 15
Human fatty acid binding protein homologue (PA-FABP)

FIG. 6E



M62403
J04093
X12876
L19686
AC002115
M55409
U12404
Z28407
X93036
X98482
X82693
AF000562
U16799
X54232
J02874
L76568
M65292
L33842
U24389
X76180
D63475
D16480

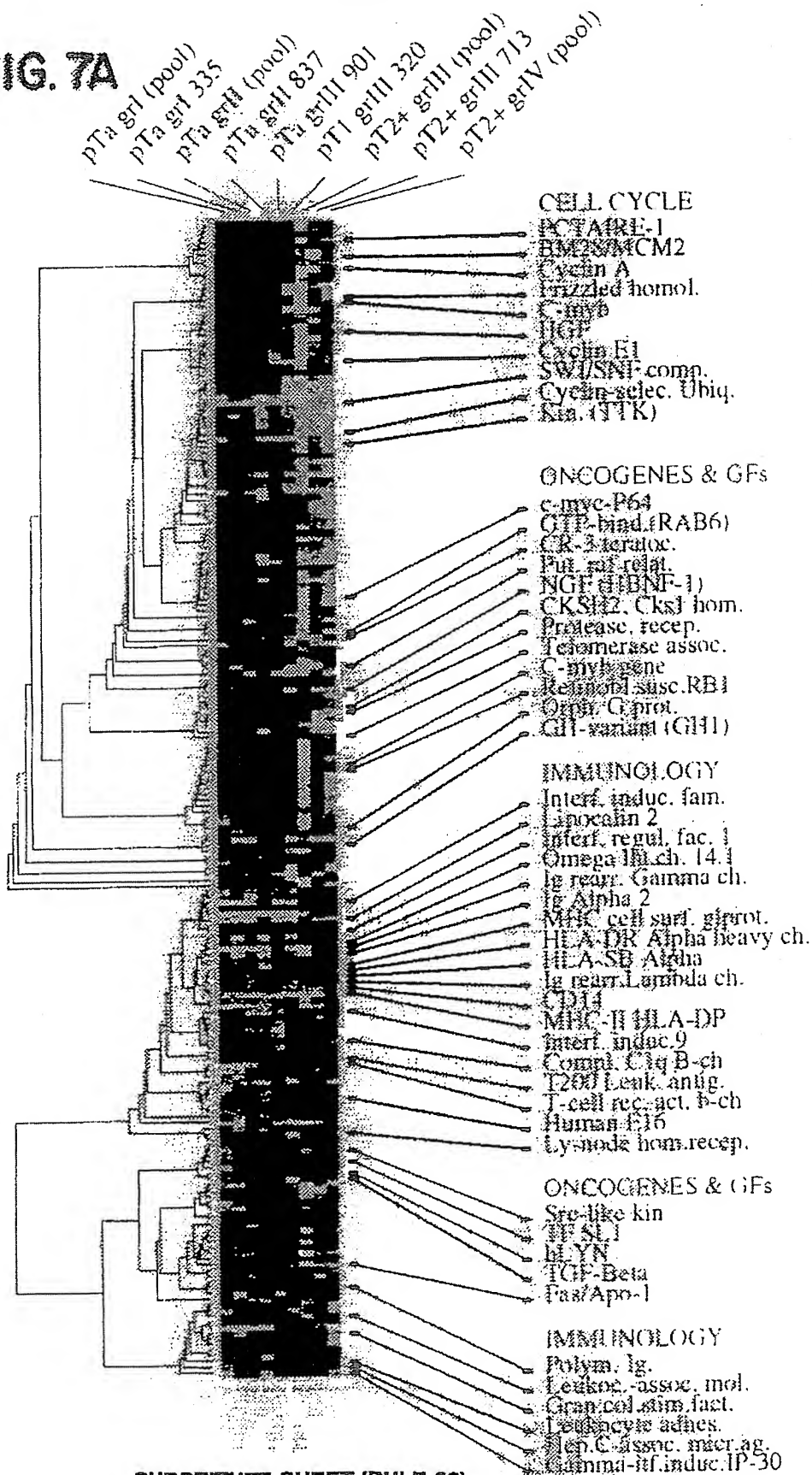
Invasive TCC related genes

E.

Insulin-like growth factor binding protein 4 (IGFBP4)
Phenol UDP-glucuronosyltransferase (UDPGT)
DNA seq. From RP3-474112 on chromosome 22q13.1-13.2
Macrophage migration inhibitory factor
DNA from chr. 19 cosmids R31396, F25451, and R31076
Pancreatic tumor-related protein
Human Csa-19
MRNA for ribosomal protein L8
MRNA for MAT8 protein
TNNT2 gene exon 11
MRNA for E48 antigen
Uroplakin II
Na,K-ATPase beta-1 subunit
MRNA for heparan sulfate proteoglycan (glypican)
Adipocyte lipid-binding protein
S26 from excision and cross link repair protein (ERCC4)
Human factor H homologue
Type II inosine monophosphate dehydrogenase (IMPDH2)
Lysyl oxidase-like protein gene
MRNA for lung amiloride sensitive Na⁺ channel protein
MRNA for KIAA0109
Mitochondrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase

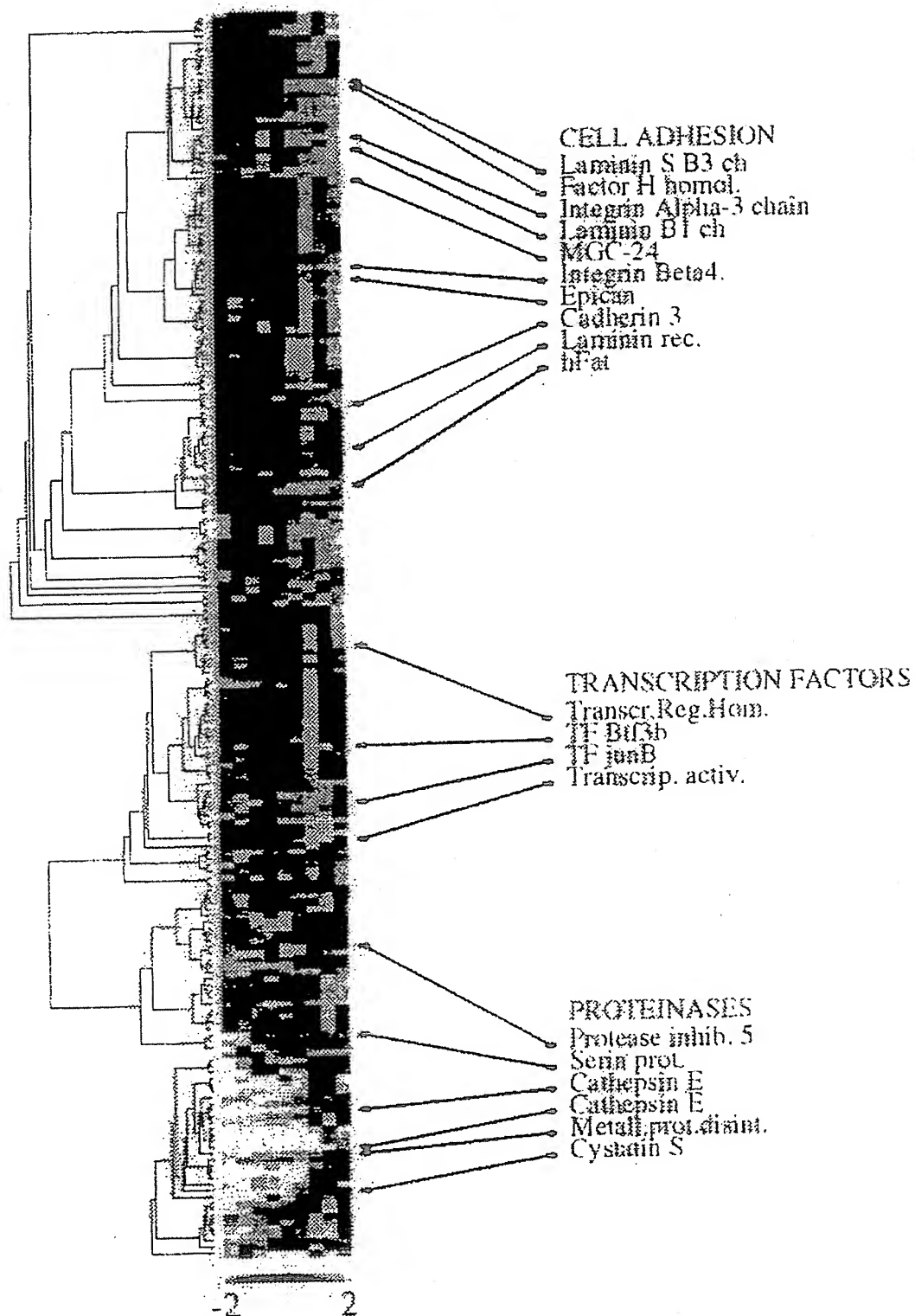
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FIG. 7A



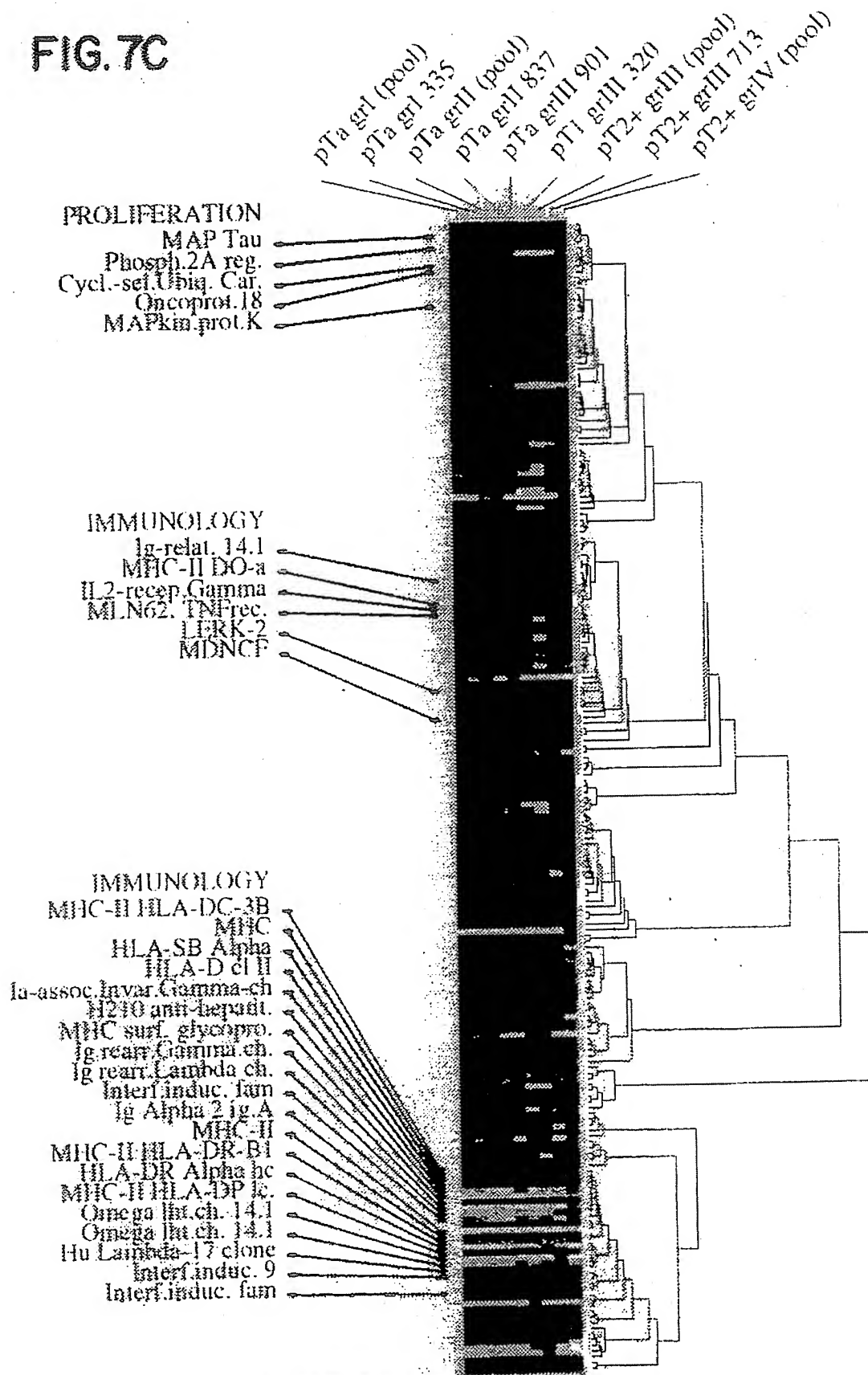
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FIG. 7B



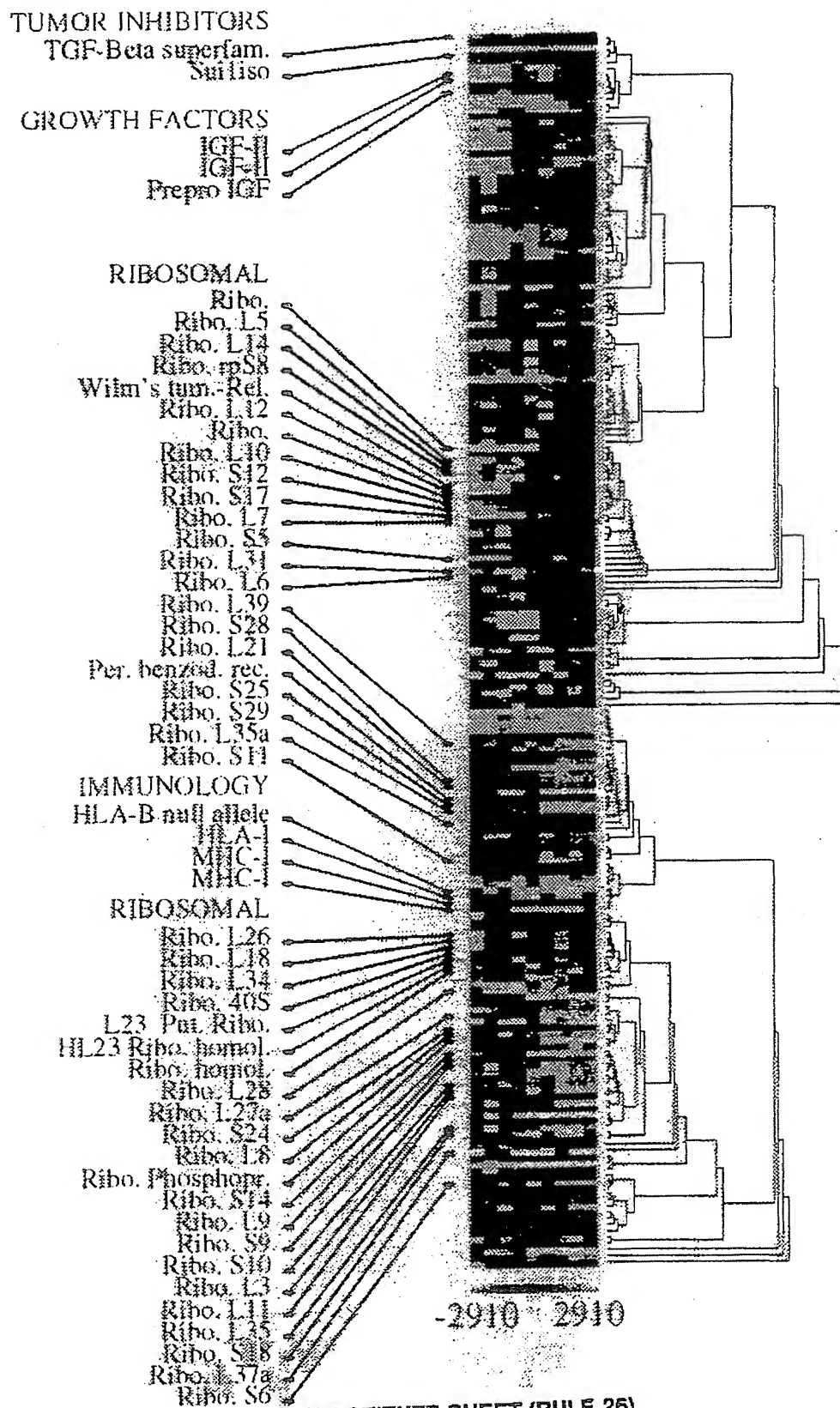
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FIG. 7C



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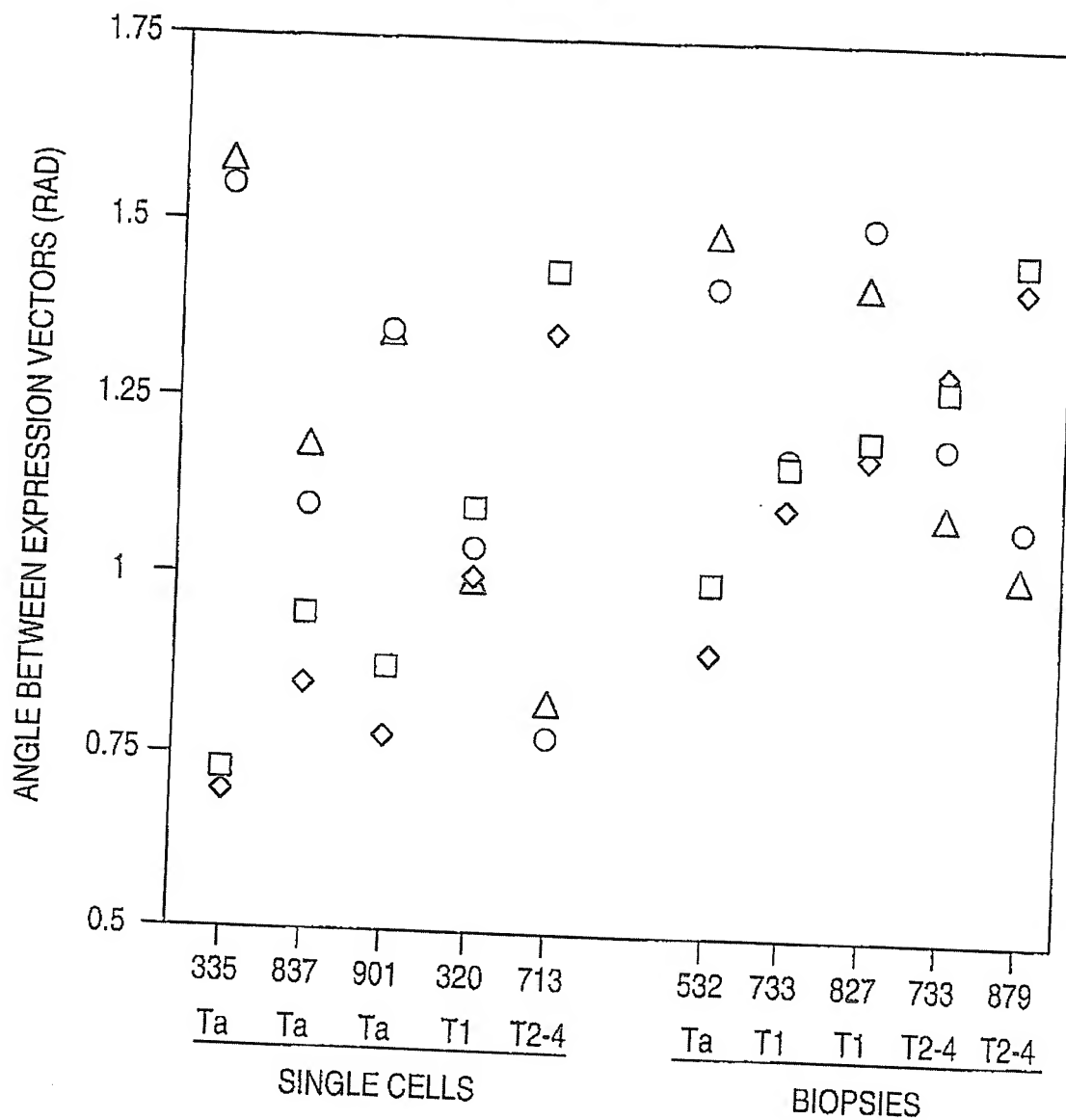
FIG. 7D



SUBSTITUTE SHEET (RULE 26)

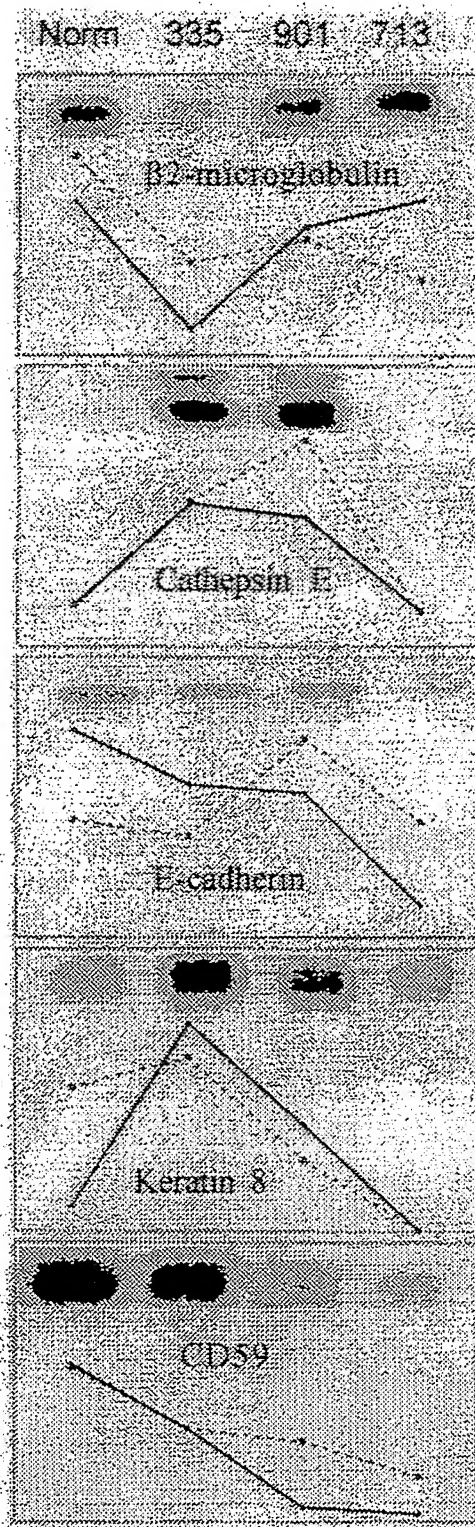
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FIG. 8



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FIG. 9



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FIG. 10



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Fig. 11 was missing at the time of publication